SUMMARIES

DB

Length

Query

AKO01621 Home sapi BC001222 Home sapi BC017899 Home sapi BC012152 Home sapi BC012152 Home sapi AK775811 Sequence AK122896 Home sapi BC049095 Mus muscu AK125034 Home sapi BC060625 Mus muscu AK122101 Home sapi BC01375 Mus muscu BC01375 Mus muscu BC012142 Mus muscu BC021442 Mus muscu BC050552 Home sapi BC056565 Mus muscu BC056666 Home sapi BC056666 Home sapi

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            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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AV112736 Rattus no AV112740 Rattus no AV12738 Rattus no AL834500 Homo sapi AV112737 Rattus no AL83294 Homo sapi BC060607 Mus muscu

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ALB34312 Homo sapi AB088091 Homo sapi AC001050 Homo sapi BX647231 Homo sapi

ALIGNMENTS

AX747350 Sequence
AX092089 Homo sapi BC054513 Homo sapi X74855 M.musculus AJ012164 Casuarina BC053915 Danio rer AF132159 Drosophil BC014276 Homo sapi AX051427 Drosophil BC031460 Mus muscu AX112736 Rattus no AX112736 Rattus no AX112740 Rattus no

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PAT 16-AUG-2002 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. linear DNA Xillary,A., Chandler,D. and Lott,S.
The tumor suppressor car-1
Patent: WO 0212285-A 3 14-FEB-2002; 3826 bp Sequence 3 from Patent W00212285. AX491279 AX491279.1 GI:22323980 Homo sapiens (human) Homo sapiens DEFINITION ORGANISM REFERENCE AUTHORS TITLE JOURNAL

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3120 CTGGAGGAGTGGCAAGACTGAGCCTAAATGTCTCCCCGGCCTTTTTTTT	BC001222 3259 bp mRNA linear PRI 04-OCT-2003 W Homo sapiens hypothetical protein FLJ10759, mRNA (cDNA clone MGC:938 IMAGE:3355572), complete cds. BC001222 BC001222.1 GI:12654758 MGC. Homo sapiens (human)	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoscomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  1 (Dases 1 to 3259) Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altechul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Blat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubinin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bondlow,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abraman,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,	Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Worllalon, D.K., Muzny, D.M., Sodergren, E.J., Lux, Gibbs, R.A., Villalon, D.M., Muzny, D.M., Sodergren, E.J., Lux, Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whitling, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.W., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)	
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	RESULT 5 BC001222 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS	TITLE JOURNAL MEDLINE	REFERENCE AUTHORS TITLE JOURNAL REMARK COMMENT
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                                                                                                                                                                                           Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LINL at: http://image.llnl.gov
Series: IRAL Plate: 6 Row: J Column: 17
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 8922647.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / translation="MACSLKDELLCSICLSIYODPV3LGCEHYFCRRCITEHWVROER OGARDCPERCRETEREPHAPSLATANIVERYSER OGARDCPERCRETEREPHAPSLATANIVERYSERPEDAILMARRAARPCQAHDKVKLF CLTDRALLCFFCDFALHEQHQYTGIDDAFDELQRELKODLQALGOSERFHTBALQLL KRQLAETKSSTKSETRIHGLRERQKAMLEELAADTAFTLJUDISQKVQRY SQQLRKVOESAQILQERLAETDRHTFLAGVASLSERKGKHHETNLTYEDFFTSKYTG PLQYTIWKSLFQDIHPVPAALTLDFGTAHQRLILSDDCTIVAYGNLHEPQPLQDSFRRF DVEVSVLGSBAFBSGYNTWEVVVARKCQWYGLAEPBAASRKSIQIQPSRGFYCIVMH DGNQYSACTEBWTRLNVRDKLDKVGVFLDFTSQCGLLIFYNADDMSWLYTFREKFPGKLC
BC Cancer Agency, Vancouver, BC, Canada info@bcgsc.bc.ca Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Mess, Pawan Pandoh, Anna-Lissa Prabhu, Parvaneh Seedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
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/note="SPRX; Region: Domain in SPla and the RYanodine
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/note="BBC; Region: B-Box C-terminal domain"
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/db xref="G1:12654759"
                                                                                                                                                                                                                                                                                                                                                                                       /tissue type="Eye, retinoblastoma"
/clone_lib="NIH MGC_16"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64. .192
/note="RING; Region: Ring finger"
dob_xref="CDD:smart00184"
445. .798
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MGC:938 IMAGE:3355572"
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/db_xrref="CDD:smart00449"
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913_.1074
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/db_xref="LocusID:55223"
                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pOTB7"
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Colonia   Colo	ACCESSION BC007999 VERSION BC007999.1 GI:14124949 KEYWORDS MGC.
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/db_xref="LocusII:55223"
/translation="MACSLKDELLCSITQDPVSLGCEHYFCRRCITEHWVRQEA
OGARDCPECRRTFAEPALAPSLKLANIVERYSFSFLDAILINRRAARFOQAHDKVKLF
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KRQLAETKSSTKSLRTTIGEAFERLHRLLRERQKAMLEELEADTARTLTDIEQKVQRY
SQCLRKVGRSGAQILQERLAETDRHTFLAGVAELSERLKGKTHETNLTYEDFFTSKYTG
PLQYTIWKSLFQDIPHEYPAALTLDPGTAHQRLILSDDCTIVAYGNLHPQPLGDSFKRF
DVEVSYLGSEAFSSGVHYWEVVVAEKTQWYIGLAHEAASRKSSIQIQPSEKGFYCIVMF
DONGVSAGTEWTELMYRELDKENGWYGLILSDCTIVAYGNLHPQPLGDSFKRF
DONGVSAGTEWTELMYREKLDKVGRYTELDYDQGLLIFYNADDMSWLYTFREKFPGKLC
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/db xref="CDD:smart00589"
1075. .1413
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/note="RING; Region: Ring finger"
/bo.xref="CDD:smart00184"
445. .798
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/note="BBC; Region: B-Box
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                                                                                                                                Strausberg, L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Colling, F.S., Magner, L., Schmefer, C.F., Bhat, N.K., Altschul, S.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marushna, K., Farmer, A.A., Rubin, G.M., Hong, L., Staoleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Carninoi, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.M., McKenn, R.J., Mallah, S.J., Hulyk, S.W., Worley, K.C., Hale, S.J., Garcia, A.M., Gay, L.J., Hulyk, S.W., Vilalon, D.K., Muzny, D.M., Soderspren, R.J., Lu, X., Gibbs, R.A., Kalhalo, S., Garcia, A.M., Madan, A., Rodriques, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y. Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Garen, E.D., Dickson, M.C., Rodriquez, A.C., Grimwood, J.S., Schmer, D.E., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov
Series: IRAL Plate: 23 Row: a Column: 20.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Info@boggs.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Radaman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Letticia Hsiao, Martin Kzzywinski, Reta Kutsche, Oliver Lee, Son
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jaqueline
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
                                   Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (15-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human and mouse CDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL.) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada
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/product="hypothetical protein FLJ10759"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue type="Eye, retinoblastoma"
/clone_lib="NIH_MGC_16"
/lab_host="DH10B-R"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="Vector: pOTB7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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       Homo sapiens (human)
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Direct Submission
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                                       ORGANISM
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TITLE
JOURNAL
                                                                                                                                       REFERENCE
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COMMENT
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Galthersburg, Maryland;

Web site: http://www.nisc.nih.gov/
Contact: nisc mgcahngri.nih.gov
Contact: nisc mgcahngri.nih.gov
Akhter.N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Madurco,O.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clone distribution: MGC clone distribution information can be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QGARDCPECRRTFAEPALAPSLKLANIVERYSSFPLDAILNARRAARPCQAHDKVKLF
CLTDRALLCFFCDEPALHEQHQVTGIDDAFDELQRELKDQLQALQDSEREHTEALQLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KRQLAETKSSTKSLRTTIGEAFERLHRLLRERQKAMLEELEÄDTÄRTLTDIEQKVÖRY
SQQLRKVQEGAQILQERLAETDRHTFLAGVASLSERLKGKIHETNLTYEDFPTSKYTG
PLQYTIWKSLFQDIHPVPAALTLDPGTAHQRLILSDDCTIVAYGNLHPQPLQDSPKRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MACSLKDELLCSICLSIYQDPVSLGCEHYFCRRCITEHWVRQEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DVEVSVLGSEAFSSGVHYWEVVVAEKTQWVIGLAHEAASRKGSIQIQPSRGFYCIVMH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               through the I.M.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 27 Row: b Column: 5 at: http://image.llnl.gov
This clone was selected for full length sequencing because it
passed the following selection criteria: Similarity but not
identity to protein.
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                                                                                                                                                                                                                                                                             cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
NIH-MGC Project URL: http://mgc.nci.nih.gov
On Dec 19, 2003 this sequence version replaced gi:15079757.
Contact: MGC help desk
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/db_xref="EDD:smart00502"
913..1074
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/clone_lib="NIH_MGC_16"
/lab_host="DH10B-R"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Young, A., Zhang, L.-H. and Green, E.D.
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/db_xref="LocusID:55223"
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445. .798
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                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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/gene="FLJ10759"
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           REMARK
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Rlausberg, R.L., Feingold, E.A., Grouse, I.H., Derge, J.G.,
Rlausberg, R.L., Zeeberg, B., Buetrow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Max, S. I., Mang, J., Haieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Male, Z., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Vilalon, D.K., Malay, J.A., Gunaratne, P.H., Richards, S.,
Rorley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Vilalon, D.K., Wairing, M., Sodergren, B.J., Lu, X., Gibbs, R.A.,
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Generation and mouse cDNA sequences
M.D. Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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<i>&amp;</i> 8	1951 TGCTCTTACTTCAGCCCTGGCCAGAGCCACGCCAATGGCAAGAACGTTCAGCCGCTGCGG 2010
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                                                                                                        GAGCGGGAACACACCGAAGCGCTGCAGCTGCTCAAGCGACAACTGGCGGAGACCAAGTCT
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Series: IRAL Plate: 29 Row: d Column: 2
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 8922647.
Location/Qualifiers
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/protein_id="AAH12152.1"
/db_xref="GI:15082476"
/db_xref="LocusID:55223"
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/note="SPRY; Region: Domain in SPla and
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/tissue_type="Eye, retinoblastoma"
/clone_lib="WNH MGC_16"
/lab_host="DH10B-R"
/note="UNCCLOR: POTB7"
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/note="RING; Region: Ring finger"
/Ab.ref="CDD:smart00184"
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/db_xref="LocusID:55223"
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ATCAACACCGTCCGCATCTAGTCCAGGCAGAAGGAGACCACAACCTCCTGGGACC	1560 TGGAGACCTCAGGCCAGTTGTTTACCCTCCAGCCTCGAGTCTGTAAATGGAGGTTGCAT 1619 2191 TCCCTACTTCCTAAACTCTTTCCAGCATCGAGTCTGTAGCTCTGACTTGATAGGGA 2250 1620 TCCCTACTTCCTAAACTCTTCCAGCATGTTCTGTAGCTCTGACCTTGATAGGGA 1679 2251 TACAGCTTTGATCAGGATGTACATGTTCCTCAGGGAACCCCTGCCCAACCCT 1680 TACAGCTTTGATCAGGATGTACAGGCTTCTCTCAGGGGAACCCCTGCCCAACCCT 1680 TACAGCTTTGATCCAAGGATGTACATGCTTCTCTCAGGGCAACCCCTGCCCAACCCT 1680 TACAGCTTGATCCAAGGATGTACATGCTTCTCCTCAGGGCAACCCCTAGCCCAACCCT 1739	SCCT SCCT SACCC CACCC	1859 TCTTATGLCCTAGGCTAAGACTTACCCTGACCAAGCTAGGGGTGGCCATTTACCCT 1918  2491 TGACCCCAGTCCCAGTGGTACAGGGGTACCTGGGGGTTGCCTAGGGGCAAC 2550  [1919 TGACCCCAGTCCAAGGGTAGATACCTGGTCCTAGGGTTGCCTGAGAGCCAAC 2550  1919 TGACCCCAGTCCAAGGGTAGATACGTTCCTAGGGTTGCCTGAGAGCCAAC 1978  2551 CTCTCCTGCCACCCCCAAGAACTAATAGGTTCCTAACTTCTCCCAACTGATCTG 2610	1979 CTCTCCTGCCACCCCCACCACCAAGAACTATATGGTTCCTCCACTGATCTGCTG 2038  2611 GTCAGTGATGATGCTGTGGCCTGTGGAAGGCACCTGGTAGTTCCACCACTTATAGT 2670  2611 GTCAGTGATGATGCTGTGGCCTGTGGAAGGCACCTGGTAGTTCAGTCCACACTTATAGT 2670  2039 GTCAGTGATGATGCTGTGGCCTGTGGAAGGCACTGGTAGTTGAGTCCACACTTATAGT 2098  2671 CATGTGCCACCACCACAGGCCACAGGCACAGGGTAGAGGTTATACCCAAAGCT 2730  2039 CATGTGCCACCACCACCACAGGCCAAGGGACAAGGGTATACCCAAAGCT 2158  2039 CATGTGCCACCACCACTAGCCCACAAGACAGGAAGGCTCCCTGGATGACCAAAGCT 2730		2971 AACAAGAGCCACTTGTAGCTGGTTTAATTAGACAAGGATTTACTACCTGGCCCCTGGTGG 3030 2399 AACAAGAGCACTTGTAGCTGGTTTAATTAGACAAGGATTACTACCTGGCCCCTGGTGG 2458 3031 CTTGCTAAATTGTTGGAAGACTGGAGAAGCAGTGTTGCTGGAATTTCCAGGAACTCCCA 3090 2459 CTTGCTAAATTGTTGGAAGAGAGAAGAGACTCTGCTGAATTTCCAGGAACTCCCA 2518 3091 GCGCCAGATTCATGTTGGAAGAGAAGAGAAGCTGCCCAATTTCCAGGAACTCCCA 2518

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PLOYTIWKSLFQDIHPVPAALTMDPGTAHQRLILSEDCTIVAYGNLHPQPLQDSFKRF
DVEVSVLGSEAFSSGVHYWEVVVAEKTQWVIGLAHEAASRKGSIQIQPSRGFYCIVMH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: Plate: Row: Column: 0.
Location/Qualifiers
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SYFSPGQSHANGRNVQPLRINTVRI"
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Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Jim Lin, University of Iowa

CDNA Library Preparation: M. Bento Soares, University of Iowa

CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)

DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thomas L. Casavant.

Cobside http://genome.uiowa.edu
Contact: bento-scares@ulowa.edu; tom-casavant@ulowa.edu
Bonaldo,M.F., Akabogu,I., Bair,T., Bair,J., Crouch,K., Davis,A.,
Fishlar,K., Keppel,C., Kucaba,T., Lebeck,M., Melo,A., Schaefer,K.,
Scheetz,T., Smith,C., Snir,E., Tack,D., Trout,K., Walters,J.,
Casavant,T., Soares,M.B.
                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (19-MAR-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Region: associated with SPRY domains" /ab xref="CDD:smart00589" / 11072. 1410 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1078 / 1
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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/note="BBC, Region: B-Box C-terminal domain"
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/etrain="c57BL/6"

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/note="RING; Region: Ring finger"
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D., Altschul, S.F., Jordan, H., Mooree, T., Max, S.I., Wang, J., Habeh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Boask, S.A., McEwan, P.J., McKernan, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Boulfand, G., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Schmutz, J., Myers, R.M., Schnern, Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
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2655 GCGCTGCAGCTGCTCAAGCGACAACTGGCGGAGACCAAG 2617
                                                           1069 GCGCTGCAGCTCCAAGCGACAACTGGCGGAGACCAAG 1107
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BC060625
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Direct Submission

Direct Submission

Direct Submission

Submitted (15-JUL-2013) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan

Bennil:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NBDO human cDNA sequencing project supported by Ministry of

Economy, Trade and Industry of Japan; cDNA full insert sequencing:

Research Association for Biotechnology (RAB); cDNA library

construction: Helix Research Institute (HRI) (supported by Japan

Key Technology Center etc.); 5- & 3-end one pass sequencing: RAB,

HRI, and Biotechnology Center, National Institute of Technology and

Evaluation; clone selection for full insert sequencing: HRI and

RAB; annotation: HRI and RAB.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ota,T., Nakagawa,S., Senoh,A., Mizuguchi,H., Inagaki,H., Sugiyama,T., Irie,K., Otsuki,T., Sato,H., Wakamatu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,T., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H., Mateuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K., Takahashi-Fujij,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MHWALTGLDGKLPSCHFLAVGLQVGPSTSLCLSCLTDKIEITTV
PTWDDFFSFLFFWFLFLLFFIFLKWSLTLVAQAGVQWLDIGSLQPPPPGFKQFSCLSL
LSSWDYRHPPPCPASFCIFSRDGVSPYWPGWS"
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                                                                                                             651
                                                                                                                                                       19 GCCCTGGCGCCATGGCGTGCAGCTCAAGGACGAGCTGCTGTGCTCCATCTGCCTGAGG
                                                                                                                                                                                                                               79 AICTACCAGGACCGGGTGAGCCTGGGGCTGCGCAGCACTACTTCTGCCGCCGCTGCATCACC 137
                                                                                                                                                                                                      652 ATCTACCAGGACCCGGTGAGCCTGGGCTGCGAGCACTACTTCTGCCGCCGCTGCATCAC 710
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                             592 GCCCCTGGCGCCATGGCGTGCAGCCTCAAGGACGAGCTGCTGTGCTCCATCTGCCTGAGC
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                 Length 3216;
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                                                                                                                                                                                                                                                                                                                                                        3444 bp mRNA linear
Homo sapiens cDNA FLJ43044 fis, clone BRTHA3003474.
AK125034
                                                           0; Indels
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/tissue type="thalamus"
/tote=lib="BRTHA3"
/hote="cloning vector: pME18SFL3"
                                                                                                                                                                                                                                                                                                                                                                                                                                          AKI25034.1 GI:34530992
oligo capping; fis (full insert sequence).
Homo sapiens (human)
                                     5.3e-54;
                 DB 10;
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3.1%; Scc. 100.0%; Pred. No. 5... 0; Mismatches
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'db_xref="GI:34530993"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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/db_xref="taxon:9606"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 4150)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Schemen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schefer, C.F., Bat, N.K., Hopkins, R.F., Jordan, H., Morce, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleron, M., Soares, M. B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Boarsk, S.A., McEwan, P.J., McKernan, K.J., Mallek, J.A., Gunaratne, P.H., Richards, S.W., Villalon, D.K., Malzk, J.A., Gunaratne, P.H., Richards, S.W., Villalon, D.K., Mairn, J.M., Sodergren, B.J., Luy, Gaby, Green, E.D., Bouffard, G.G., Blakes, Ledy, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Salska, U., Smailus, D.E., Generation and initial analysis of more than 15,000 full-length human and mouse odn. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Email: ggapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library Preparation: M. Bento Soares, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr.
Thomas L. Casavant.
Web site: http://genome.uiowa.edu
Contact: bento-soares@uiowa.edu; tom-casavant@uiowa.edu
Bonaldo,M.F., Akabogu,I., Bair,T., Bair,J., Crouch,K., Davis,A.,
Fishler,K., Keppel,C., Kucaba,T., Lebeck,M., Melo,A., Schaefer,K.,
Scheetz,T., Smith,C., Snir,E., Tack,D., Trout,K., Walters,J.,
Casavant,T., Soares,M.B.
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ROD 12-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg, R. Direct Submission Direct Submission Mammalian Submitted (31-OCT-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                  Mus musculus Inf receptor-associated factor 2, mRNA (cDNA clone MAAGE: 6631932), partial cds.
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4150 bp
                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
                                                                                                                                                                               BC060625.1 GI:38197727
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Location/Qualifiers

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Strausberg, L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, P.S., Wagner, L., Schaefer, C.F., Bhat, N.K.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.L., Wang, J., Haieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M. B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Abramson, R.D., Mallahy, S.J., Bosak, S.A., McEwan, P.J.,
Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodiziques, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Butterfield, Y.S., Krzywinski, M. I., Skalska, U., Samilus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: ang@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2619)
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Submitted (19-DEC-2001) National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
(cDNA clone MGC:30533 IMAGE:5008599), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Contal: gapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
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Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
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/gene="DlErtd622e"
                                                                                                                  Mus musculus (house mouse)
                                                            BC019375.1 GI:18043921
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The (Bases 1 to 4685)

Mambutt,R., Heubner,D., Mewee,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.

Direct Submission

Submitted (13-MAY-2003) MIPS, Ingolstaedter Landstr.1, D-85764

Neuherberg, GERMANY

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ): Email s. wiemann@dkfz-heidelberg.de; sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project.

This clone (DKFZp313H168) is available at the RZPD in Berlin. Please contact the RZPD: Reseourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/proj/CDNA/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSMB03417 4685 bp mRNA linear PRI 13-MAY-2003
Homo sapiens mRNA; cDNA DKFZp313H168 (from clone DKFZp313H168).
AL832110
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                                                                                                                                                                                                                                                                                                                                 Query Match 0.7%; Score 27; DB 10; Length 4150; Best Local Similarity 100.0%; Pred. No. 0.014; Matches 27; Conservative 0; Mismatches 0; Indels C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
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Best Local Similarity 100.0
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DEFINITION

ACCESSION

VERSION KEYWORDS

RESULT 14 HSM803417 LOCUS

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ORGANISM

SOURCE

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

FEATURES

LOCUS

RESULT 15 BC019375

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159. 702

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ORIGIN

.; 0 Query Match 0.7%; Score 26; DB 10; Length 2619; Best Local Similarity 100.0%; Pred. No. 0.051; Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps

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Search completed: September 4, 2004, 11:29:30 Job time : 9627 secs

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                                                                                                           4, 2004, 06:55:12 ; Search time 944 Seconds
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(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                               3373863 seqs, 2124099041 residues
                                                                      - nucleic search, using sw model
                                                                                                                                                                                                                                                          OLIGO_NUC
Gapop_60.0 , Gapext 60.0
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               Copyright
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Post-processing: Listing first 45 summaries

Minimum DB seq length: 2500 Maximum DB seq length: 5000

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Total number of hits satisfying chosen parameters:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

cDNA enco Human REM Human ORF Human pol Human cDN Human pro Human pro pro Human ost Drosophil DNA encod Recombina Abk12806 Human cDN Aah14509 Human cDN Nuclear f ung canc Human pro cDNA enco Clone df3 Human col DNA relat Human Human Description Abx76356
Aav82781
Abq92018
Adb62721
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Abv23296
Abv30164
Abv25571
Abv29143 Aax35727 Add69641 Aac76424 Aca98971 Ada38053 Abg88201 Ab115850 Abk99971 Aaq04043 SUMMARIES ABK12806 AAH14509 ADC37268 ABX76356 AAV82781 ABQ92018 ABV23296 ABV25449 ABV30164 ABV25571 ABV29143 AAX35727 ADB62721 AAH34824 AAQ04043 AAA35032 ADD69641 AAC76424 ACA98971 ADA38053 ABL15850 ABK99971 Length DB 4498 4572 4585 4717 4729 4740 2522 2582 2629 2647 2647 2647 2647 2647 2647 3858 3891 4493 Query Score Result 00000

Claim 2; Page 134-135; 185pp; English.

Human ade

	Abk50046 cDNA enco	Abk83766 Human cDN	Abz96848 Human nuc	Abv76142 Human Mac		Aac78146 Human can			. ,	Ada56044 Gene enco		,	Abx58777 cDNA enco	Abl10304 Drosophil	Abx63799 Human cDN	Abz18582 Group III	Aad18016 Conjothyr	_	Aah18311 Human cDN	Abl27612 Drosophil	•
AAF21154	ABK50046	ABK83766	ABZ96848	ABV76142	ADD25614	AAC78146	ADE87242	ABL21586	AAD05059	ADA56044	ADA39854	AAL35789	ABX58777	ABL10304	ABX63799	ABZ18582	AAD18016	ABA93708	AAH18311	ABL27612	AAA23433
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7.0	0.7	0.7	0.7	0.7	0.7	9.0	9.0	9.0	9.0	9.0	9.0	9.0	•	٠	9.0	٠.	•	9.0	9.0	9.0	9.0
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## ALIGNMENTS

RESULT 1

New tumor suppressor CAR-1 polypeptides and polynucleotides, useful for diagnosing cancer, for altering the phenotype of a tumor cell, for treating cancers or as a diagnostic or prognostic indicator of cancer. Human; ss; tumour suppressor; gene; CAR-1; cytostatic; cancer; tumour; gene therapy; brain cancer; lung cancer; liver cancer; kidney cancer; colon cancer; stomach cancer; breast cancer; endometrial cancer; prostate cancer; testicular cancer; ovarian cancer; skin cancer; head and neck cancer; osophageal cancer; bone marrow cancer; chromosome 1p31-1p36; Human cDNA encoding tumour suppressor CAR-1. Location/Qualifiers 604. .2031 /\*tag= a /\*tag= a /product= "CAR-1" ABK12806 standard; cDNA; 3826 BP Lott S; 09-AUG-2001; 2001WO-US025269 10-AUG-2000; 2000US-0225033P. 23-AUG-2000; 2000US-0227560P. (first entry) (TEXA ) UNIV TEXAS SYSTEM Chandler D, WPI; 2002-269088/31 P-PSDB; AAU78657 WO200212285-A2 Homo sapiens 18-JUN-2002 Killary A, ABK12806: ABK12806 

The invention relates to an isolated polymucleotide encoding a
polypeptide being tumour suppressor, CAR-1. Also included are fragments
of the polymucleotide from 15-500n nucleotides, fragments of the protein
from 10-50 aminon acids, an expression cassette comprising the
cells, a method for suppressing growth of a cancer cells by contacting
the cells with the expression cassette (i.e. gene therapy), a cell
comprising the expression cassette, an anti-CAR-1 moncolonal or
comprising the expression cassette, an anti-CAR-1 moncolonal
antibody, a method of diagnosing a cancer by assessing the expression of
cattleotid antibody, a method of antibody of a tumour suppressor CAR-1 and
cattleotid for altering the phenotype of a tumour suppressor CAR-1 and
cattleotid for altering the phenotype of a tumour suppressor CAR-1 and
cattleotid for the region encoding the tumour suppressor CAR-1 and
concer active in enkaryotic cells, where the promoter is operably
concerned active in enkaryotic cells, where the promoter is operably
concerned activity by contacting a cell lacking functional CAR-1 gene, a non-human
cransgenic enkaryote that over-expresses CAR-1 as compared to a similar
con-transgenic enkaryote that over-expresses CAR-1 as compared to a similar
con-transgenic enkaryote the contacting a cell lacking functional CAR-1 polypeptide, with a candidate substance and determining the effect of the
candidate substance on the cell, an anti-tumour composition produced by
contacting a cell lacking functional CAR-1 polypeptide, with a candidate
contacting a cell lacking functional contacting a candidate substance
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contacting a cell lacking functional contacting contacting a candidate contacting a cell acking the effect of the candidate substance
co chromosome 1 (1p31-1p36). The present sequence is the cDNA encoding CAR-1 invention relates to an isolated polynucleotide encoding a 

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Gaps . 0 Sequence 3826 BP; 797 A; 1286 C; 999 G; 744 T; 0 U; 0 Other; Indels . 9 . DB Score 3826; I Pred. No. 0; ; Mismatches 0; 100.0%; Conservative Best\_Local Similarity Matches 3826; Conserv Query Match

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240 240 360 360 420 420 180 300 180 9 rreascrecceacracereragaerecerecereceresecresecreceses GCTTCTCGCCCTCCCCGCACCGCCCCCACCCGGGATTTCGACCCCCTTAAGGGCTCCAC CCCGCTCCGGGATCCCCTTCCCCAGCTCCTTATCCCTTAGGACTGCCCCGCCCCTAGAA cecerrecessariecerrereceaserecrarecerrassacreceeeeerasaa cencecedencidadan crecencide de concade concence de concene de con TIGAGCIGCCACTACCICIAGACIGCCCICCCGGGCIGCCGICCCACGGAGICICAGCC CCTCCCCCTCAGGATCTCCCTCCACCCCTCACAGCCTCCTCCTCCCAGCGCCCCATCGCC CCAGGGTTTGGGGCCGGGATCCGGCAGCTGAGCGGGCCGGCACCCCTCTTCTCTCTGCC GGTCACAGCCAATGTACGGCTCGGCCTGCCCCCTCCCCCAGGATTCCCCATCCCCA GCTTCTCGCCCTCCCCCCCCCCCCCCCCCGGGATTTCGACCCCCTTAAGGGCTCCAC AGGCTGCGCTGGACCGAAGCGGTGGCTAAGCTCGCGGGGGTAAGGGGGTCGCGCTGGG 1 AGGCTGCGCTGGACGGAAGCGGTGGCTGCTAAGCTCGCGGGGTAAGGGGTCGCGTGGG 361 421 301 301 61 61 121 121 181 181 241 241

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480 540 540 009 009 099 099 720 720 780 780 840 840 900 900 096 960 GACCCGGGCACAGCCCACCAGCGCCTGTCGGCGCGCGCCCCCTTGTGGGCTTAC GAGGCCTTCGAGCGGCTGCTGCTGCTGAACGCCAGAAGGCCATGCTAGAGGAG CTGGAGGCGGACACGCCCGCACGCTGACCGACATCGAGCAGAAAGTCCAGCGTACAGC criciangecidancacececececricaceacarecanecagadaaagrecageceracage CATGAGACCAACCTCACATATGAAGACTTCCCGACCTCCAAGTACACAGGCCCCCTGCAG TACACCATCTGGAAGTCCCTGTTCCAGGACATCCACCCAGTGCCAGCCGCCCTAACCCTG GAGGCCTTCGAGCGGCTGCACCGGCTGCTGCGTGAACGCCAAGAAGGCCATGCTAGAGGAAG GACCGGCACACCTTCCTGGCTGGCCTCACTGTCCGAGCGGCTCAAGGGAAAAATC 1321 GACCGGCACACCTTCCTGGCTGGGCTGCCTCACTGTCCGAGCGGCTCAAGGGAAAAATC GACCCGGTGAGCCTGGGCAGCACTACTTCTGCCGCCGCTGCATCACGGGCGAGCACTGG CTGGACGCCATCCTCAACGCGCGCGCGCGCGCGCGACTCCTGCCAGGCGCACAAGGTC AAGCTCTTCTGCCTCACGGACGGCGCTTCTCTGCTTCTTCTGCGACGAGCCTGCACTG **AAGGACCAACTTCAGGCCCTTCAAGACAGCGGGGAACACACCGGAAGGCGCTGCAGCTG** caecaecrececaagerccaggaggaggcccagarccrecaggagcggcregcreargaaacc rccráccerecererecesecerestes de aseceres de GOGCOGCOLCICICAGCOGCOCCCTGCCCCTCGGGCCCCCCCTCTCTGCTGCCCTGCTGGCC GCCATGGCGTGCAGCCTCAAGGACGAGCTGCTGTGCTCCATCTGCCTGAGCATCTACCAG GTGCGGCAGGAGGCGCGCGCGCGGACTGCCCCGAGTGCCGGCGCACGTTCGCCGAG gracededagadescecadadescecescaacracecesaareceedescaestreeceade CCCGCGCTGGCGCCCAGCTCAAGCTGGCCAACATCGTGGAGCGCTACAGCTCCTTCCCG chddacdcchchancdcdcdccacacacacacacacaagacaacacacaaagacaaagacaagacaaagacaaagacaa AAGCTCTTCTGCCTCACGGACCGCGCGTTCTCTGCTTCTTCTGCGACGAGCCTGCACTG CTCAAGCGACAACTGGCGGAGACCAAGTCTTCCACCAAGAGCCTGCGGACCACTATCGGC recracecraceratecasacerearaceasacereasacereasaca dedecedes en en estados estados estados estados estados en en entra estados estados en entra en entra GACCCGGTGAGCCTGGGCTGCGAGCACTACTTCTGCCGCCGCTGCATCACGGAGCACTGG 1261 1381 1441 1021 1081 1081 1141 1201 1201 1261 1321 1381 1441 901 1021 841 901 961 196 1141 781 841 481 481 541 541 601 601 661 661 721 721 781 121

2641 CACCTGGTAGTTGAGTCCACATTATAGTCATGTGCCACCACCTTCCTGCCCACAGGCC 2700	2701 GAGGGACAGGGTGAGGGTATACCCAAAGCTGATGCAGGCCCATTAGCCTAAAAGCAACT 2760 	GCAGGACAAGCCTCCCTGGATGATCGAGGTCCCCAGTAGCTCTGAACAAGAGTCCAGCCA 282 	21 ACCTUTTCAGCCAGGCCTCTGTGACCTGCTAGGGGGGGGGG	881 TIGTAATTAGGACCCAAGCACTGGGAGGGGCTGTTGGCTACACCCCTTGTCACACTTGGC 	ATCTATCTCAGTTAGGATCCTGCAGAAAACAAGAGCCACTTGTAGCTGGTTTAATTA 3 	GACAAGGATTIACTRACCTGGACCCCTGGTGGCTTGCAAAATTGTTGGAAGAAGCTGGAGAGG 306 	CAGACTCTGCTGATTTCCAGGAACTCCCACGCCAGATTCATCATGTTGTGTGCTGCTGCTGTGTGTG	21 GGAAAGCTGCCCCCATCTGCAGGAAGCCACTATGCCAGAAAGCTGCTGACTGCAGAACTA 318 	GGCTCCCTCTGCCACGCTCCCTGCCAGCCATAGATGTCCTGAGGCCTGCCCCTCTCCCAAAAAAAA	3241 CTTCACTCAGTTCCCAAATCTAAATTTTACAAGAGATTCTGTTTGGGGGAACTTAAGTC 3300 	01 AGATCCAGAACCTTGGCTGCAAGGGAGTCTGGGAAATGTCATTTCCCTAGAAGGAAG	GGGTGGGTGGAGCAGCCCACCTGCTTTTTCTGCCACAGCATCCAATGGTGAAGAACT	21 CGGAGAGGGTGGAGTCCACATCTAGGGTTGTCCTGCCCCTTGGCTCTATCCTGCCCAG 3	3481 AGGTGGGAACTGGAGGAGTGGGCTGCAACTGAGCCTAAATGTCTCCCCGGCCTTGACT 3540 	ACAACA          ACAACA	CCAAAGTAGCCGGAAGAGCTAAACACAGGGGTTCTTAAAATGGCTGCCCCGCCACCCG 36	661 GGCCTCCCTTGGGCAAAAGGAATTGTCAGCCCTACCCCAACCCTTCAACTACCAGAATCT 372.
О	cy Dp	८० वि	& 43 €	oy Oy	oy Q	yo da	& ଶ	À 93	& 43	& a	ද්ර අධ	ද්ර අධ	∂ යි	y d	AQ Pa	À 8 8	· 원
1501 GACCCGGGCACCACCACCACCAGGTCCTGTCGGACGACTGCACCATTGTGGCTTAC 1560 1561 GGCAACTTGCACCCACACACTGCAGGACTCGCCAAAGCGCTTCGATGTGGAGGTGTCG 1620 1561 GGCAACTTGCACCCACACACTGCAGACTCGCCAAAGCGCTTCGATGTGGAGGTGTCG 1620	GTGCTGGGTTCTGAAGCCTTCAGTAGTGGCGTCCACTACTGGGGTTCGGGTTCTGGAAGCCTTCAGTAGTGGCGTCCACTACTGGGAAGTTCGGAAGCTTCCAGTAGTGGCGTCCACTACTGGAAGTTCTAGTAGTGGTCTTCCAGTAGTGGCTTCCAGTAGTGGAAGTTCTAGTAGTGGAAGTTCTAGTAGTGAAGTTCTAGTAGTGGAAGTTCTAGTAGTGGAAGTTCTAGTAGTGGAAGTTCTAGTAGTGGAAGTTCTAGTAGTGGAAGTTCTAGTAGTGGAAGTTCTAGTAGTGGAAGTTCTAGTAGTGGAAGTTCTAGTAGTGAAGTAGTGAAGTAGTAGTAGTAGTAGTAGTAG	AAGACCCAGTGGGTGATCGGGCTGGCACACGCAAGCCGCAAGGGGCAGGGCAGCATCCAG 17	1741 ATCCAGCCCAGCGCGTTCTACTGCATGGAGGCAGCGAGCAGCAGCAGGGCC 1800 	1801 TGCACGGAGCCCTGGACGCGGCTTAACGTCCGGGACAAGCTTGACAAGGTGGGTG	1861 CTGGACTATGACCAAGGCTTGCTCATCTTCTACAATGCTGATGACATGTCCTGGCTCTAC 1920 	1921 ACCTTCCGCGAGAAGTTCCCTGGCAAGCTCTGCTCTTACTTCAGCCCTGGCCAGGCCAC 1980 	1981 GCCAATGGCAAGAACGTTCAGCCGCTGCGGATCAACACCGTCCGCATCTAGTCCAGGCAG 2040 	<b>4</b> 4	2101 AAGACCTGGACTCCAGCCCACCGTGGCCACTGGAGACCTCAGGCCAGTTGTTTACCCTCC 2160 	2161 AGCCTCCAGTCTGTAAAATGGAGGTTGCATTCCCTACTTCCTAAACTTCTCTTCAGCATC 2220 	GATGTTCTGTAGCTCTGACCTTGATAGGGATACAGCTTTGATCCDAGGATGTGACATGGC	2281 TICTCCTCAGGCAACCCTGCCAACCCTCATCCCCATCTTCTCAGGGGCAGGGACTA 2340 	CCTTCCAGTGTCTCCCTCCAGCCCAGCCCTGACCAGGAAGTGTCAGAGCATGGCCAGT 24	2401 AGTIGGCAGCCGAAAGACACACACCTCTIAIGTCCCAIGGCCTAAGACTIACCCC 2460 	TGACCAAGCTAGTGATGGGCCATTTACCCTTGACCCAGTCCAGGTGGTCACAGGTAGT 25	ACCTGGTCCTAGGGTTGCCTGAGGCCAACCTCTGCCACCCCCCACACAGAACTAT 2	2581 ATGGTTCCTACTTCTCCCACTGATCTGCTGGTCAGTGATGATGCTGTGGCCTGTGGAAGG 2640 

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Length 3436;

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The present invention describes primer sets for synthesising 5602 full-
length cDNAs defined in the specification, Where a primer set comprises:
[a) an oligo-dr primer and an oligonucleotide comprises one of the 5602
complementary strand of a polyuncleotide which comprises one of the 5602
nucleotide sequences defined in the specification, where the
complementary strand of a polyuncleotide which comprises a 5'-end
complementary strand of a polyuncleotide which comprises a 5'-end
complementary strand of a polyuncleotide which comprises a 5'-end
complementary strand of a polyuncleotide which comprises a 5'-end
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complementary strand of a polyuncleotide on the
complementary strand of a polyuncleotide on the 6'-end
complementary strand of the abnormality of the proteins encoded by
the full-length cDNAs. The primers are also useful for the
detection and/or diagnosis of the abnormality of the full-length
contagnosis and sequences; AAH3632 represent human amino acid sequences; and AAH3632 represent
coligonal course.
                                                             GGGCCACCCCAGCAGTATTTTTATTTAAAATGTTGCCCATTTTATGAGTTATGATT 3780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primer sets for synthesizing polynucleotides, particularly the 5602 full-
length cDNAs defined in the specification, and for the detection and/or
diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; SEQ ID NO 12036; 2537pp + Sequence Listing; English.
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Otsuki
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A, Nagai K,
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11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
99-JUN-2000; 2000JP-002418997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to novel proteins and their coding sequences (ADC37168-ADC37455), which activate nuclear factor kappa B (NF-kappaB). The proteins and their coding sequences are useful for treating a disease associated with NF-kappaB activation, such as inflammation, autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS, neurodegenerative diseases, or ischaemic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New purified protein that activates nuclear factor kappa B (NF-kappaB) useful for treating inflammation, autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS, neurodegenerative diseases o
                              CCGGAAGACTAAAACACAGGGGTTCTTAAAATGGCTGCCCCCGCCACCGGGCCTCCCT
                                                           TGGGCAAAAGGAATTGTCAGCCCTACCCCAACCCTTCAACTACCAGAATCTGGGCCACCC
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05-DEC-2001; 2001JS-0335829P.
03-OCT-2002; 2002JP-00291302.
04-OCT-2002; 2002JS-0415769P.
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Sequence 3243 BP; 715 A; 1023 C; 863 G; 642 T; 0 U; 0 Other;

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Qy Dp

Secreted protein, nutritional activity, immune stimulating; vaccine, suppressing activity, haematopoiesis regulating activity, tissue growth activity, activin; inhibin activity, chemcactaxis, themokinetic activity, haemostasis, thrombolytic activity, receptor, ligand, anti-inflammatory, cadherin, tumour invasion suppressor;

tumour inhibition; gene therapy; ds.

Homo sapiens WO9842739-A2

Clone df396\_1 isolated from human adult brain cDNA library.

(first entry)

25-FEB-1999

AAV82781;

ga

ВР

AAV82781 standard; cDNA; 2522

AAV82781 ID AAV

RESULT

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Lung cancer-associated polynucleotide, gene, ds, cytostatic, emphysema, antiinflammatory, antiasthmatic, non-small cell lung cancer; atelectasis, small cell lung cancer, benign lession, precancerous lesion, bronchitis; chronic obstructive pulmonary disease, hypersensitivity pneumonitis; interstitial pulmonary fibrosis; fibrosis, asthma, bronchiectasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polymoclectide that exhibits increased or decreased expression in lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4702 BP; 1159 A; 1218 C; 1217 G; 1108 T; 0 U; 0 Other;
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100.0%; Pred. No. 11;
iive 0; Mismatches 0; Indels
                                                                                                Lung cancer-associated polynucleotide #220.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 22; Page 355-356; 453pp; English.
                        ABX76356 standard; DNA; 4702 BP.
                                                                                                                                                                                                                                                                                                18-APR-2001; 2001US-0284770P.
10-MAY-2001; 2001US-0290492P.
09-NOV-2001; 2001US-039245P.
13-NOV-2001; 2001US-035666P.
29-NOV-2001; 2001US-0334370P.
                                                                                                                                                                                                                                                                                                                                                                                        (EOSB-) EOS BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                                                                12-APR-2002; 2002US-0372246P.
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                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                  Murray R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; ABU56627.
                                                                                                                                                                                                                          WO200286443-A2.
                                                                                                                                                                                                  Unidentified
                                                                         02-APR-2003
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                                                 ABX76356;
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RESULT 4
             ABX76356
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Treacy M;

Jacobs K, Mccoy JM, Lavallie ER, Racie LA, Merberg D, Spaulding V, Agostino MJ;

WPI; 1998-609890/51.

(GEMY ) GENETICS INST INC.

21-MAR-1997; 20-MAR-1998;

19-MAR-1998;

98WO-US005653. 97US-00822167 98US-00044466

01-OCT-1998

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transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits to a sequence that is at least 80 % identical to a gene that exhibits in creased or decreased expression in lung cancer samples. Lung cancer compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated polypeptide, for cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful for treating a modulatory compound identified. The methods are useful for treating lung cancer, or other benign or precancerous leatons, e.g. atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and for treating and polypeptides are useful for diagnostic purposes and as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences and ast targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences
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Best Local Similarity 100.0%; Pred. No. 28;
Matches 25; Conservative 0; Mismatches
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3801 GATGTCAAAAAAAAAAAAAAAAA 3826

Conservative

Local Similarity nes 26; Conserva

Matches

Query Match

Gaps

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100.0%; Prec. ...

Conservative

25;

2495 ATGTCAAAAAAAAAAAAAAAAA 2519

0.7%; Score 25; DB 6; Length 2522;

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The invention relates to human secreted or transmembrane protein (1), their fragments and is encoded by specific complementary deoxyribonucleic acid (CDNA) inserts (11), where the protein is substantially free from other mammalian proteins. (1) are useful for preventing, treating or ameliorating a medical condition, especially immunological treatment or prevention of tumours. (1) exhibits activity relating to angiogenesis, cytokine, cell proliferation, cell differentiation, antiniflammatory, stem cell growth factor activity and activin or inhibin-related crise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or cells damaged by illness, autoimmune disease, accidental damage or cells damaged by illness, suctions of neural cells and creatment of regeneration of nerve and brain tissue and is useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's, parkinson's disease, Huntington's disease, amyotrophic activity, regulation of haematopolesis and is useful for treating myeloid cor lymphoid cell disorders, platelet disorders such as thromboxytoppenia and for recentral and cell disorders, platelet disorders such as thromboxytoppenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth and in tissue repair, healing of burns, incisions, ulcers, for treating osteoporosis, osteoarthritis, bone degenerative disorders or periodontal disease. (1) is also useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, various immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel secreted or transmembrane protein and polynucleotide encoding the protein, useful for diagnosis and treatment of neurological disorders, cancer, autoimmune diseases, bone disorders and lung or liver fibrosis.
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 ABQ92018
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(TREA/)
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(EVAN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAVA/)
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autoimmune disorders e.g. multiple sclerosis, rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic reactions and conditions, such as asthma or other respiratory problems. (II) is useful to express recombinant protein, as markers for tissues in which the corresponding protein is preferentially expressed and in gene therapy. The present sequence is that of a polynucleotide of the invention Sequence 2522 BP; 558 A; 683 C; 608 G; 673 T; 0 U; 0 Other; 3802 ATGTCAAAAAAAAAAAAAAA 3826 ADB62721 standard; cDNA; 2586 BP Local Similarity Query Match ADB62721/c Matches RESULT 8888888888 ð Human, cytostatic; antirheumatic; antiarthritic; vulnerary; analgesic; antinflammatory; antibacterial; immunosuppressive; antiparkinsonian; neuroprotective; nootropic; osteopathic; haemostatic; vasotropic; antiulcer; fungicide; antidabetic; antiasthmatic; antiallergic; immunostimulant; antiparasitic; secreted protein; transmembrane protein; cytokine; cell proliferation; cell differentiation; autoimmune disease; stem cell; growth factor; nervous system disease; neuropathy; Alzheimer's disease; Parkinson's disease; Huntington's disease; osteoporosis; severe combined immunodeficiency; SCID; infection; multiple sclerosis; rheumatoid arthritis; gene therapy; gene; ss. Evans C; Collins-Racie LA, Lavallie ER, Spaulding V; Human polynucleotide SEQ ID NO 15. 22-DEC-2000; 2000US-00745763. 98US-00040963 COLLINS-RACIE L A. EVANS C. (first entry) JACOBS K. MCCOY J M. LAVALLIE E R. Treacy M,

A, Sato H, Ishii S; ai K, Irie R, Tamechika I; Masuho Y; The invention discloses a polynucleotide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel polypeptides. Also claimed is a polypeptide encoded by the polynucleotide or its partial peptide, an antibody binding to the polypeptide or peptide of the polynucleotide, immunologically assaying the polypeptide or peptide peptide of the polynucleotide by contacting the polypeptide or peptide with the antibody of the encoded protein, and observing the binding between the two, a transformant carrying the polynucleotide in an New polynucleotides and polypeptides, useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or Human; ss; gene; pharmaceutical; diagnostic; gene therapy; tissue regeneration; cell regeneration; membrane protein; signal transduction-related protein; transcription-related protein; osteoporosis; neurological disease; cancer; tumour. /\*tag= a /product= "Clone NT2NE20028700 protein" Otsuki T, Wakamatsu A, Sa Hio Y, Otsuka K, Nagai K, Otsuka M, Nagahari K, Masu Human cDNA encoding clone NT2NE20028700. Location/Qualifiers HELIX RES INST. RES ASSOC BIOTECHNOLOGY. Claim 1; Page; 222pp; English. 28-MAR-2002; 2002EP-00007401. 05-NOV-2001; 2001JP-00379298. 25-JAN-2002; 2002US-00350978. as targets of gene therapy. 166. .1377 (first entry) Sugiyama T, J, Isono Y, Yoshikawa T, WPI; 2003-450961/43. P-PSDB; ADB64691. Homo sapiens EP1308459-A2 04-DEC-2003 07-MAY-2003. Yamamoto J, [sogai T, ADB62721; (HELI-) 1 (REAS-) 1 Seki N, 

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expressible manner and an antisense polynucleotide. The oligonucleotide is useful as a primer for synthesising the polynucleotide, or as a probe for detecting the polynucleotide. The polynucleotides and encoded proteins are useful as pharmaceutical agents and many disease-related proteins are useful as pharmaceutical agents and many disease-related genes may be included in them, for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy. The genes are involved in tissue and/or cell responsation. Membrane proteins, signal transduction-related proteins, cegeneration. Membrane proteins, disease-related proteins, centrological diseases, cancer, tumours: The cDNA may be used to regulate neurological diseases, cancer, tumours: The cDNA may be used to regulate sequence presented is a cDNA of the invention. Note: Some of the sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the Buropean Patent Office.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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28;
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Query Match
Best Local Similarity 100.0%; P1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001-235357/24
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P-PSDB; AAG75419.
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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (i) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker
to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the present invention. N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
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                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                 0;
                                                                                                                                                                            Sequence 2629 BP; 841 A; 520 C; 494 G; 773 T; 0 U; 1 Other;
                                                                                                                                                                                                              DB 4; Length 2629; 28;
                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human prostate expression marker cDNA 23287.
                                                                                                                                                                                                                         100.0%; Pred. w.-
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                                                                                                                                                                                                                 Score 25;
Pred. No.
                                                                                                                                                                                                                                                                                         3802 ATGTCAAAAAAAAAAAAAAAAAA 3826
                                                                                                                                                                                                                                                                                                             2567 ATGTCAAAAAAAAAAAAAAAAAAAA 2591
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                                                                                                                                                                                                                                                                                                                                                                                                                 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                marker; gene; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0189862P.
2000US-0207454P.
2000US-0211314P.
2000US-0219007P.
                                                                                                                                                                                                                                                                                                                                                                                                                 ABV23296 standard; cDNA; 2647
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                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pharmacogenomic
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09-JUN-2000;
18-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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us-09-927-091-3.oli18.rng

ABV30164 standard; cDNA; 2647 BP.

RESULT 11

ABV30164/

(first entry)

16-SEP-2002

ABV30164;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (1) is useful for: (a) assessing whether progression of prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate call carcinogenic potential of a compound; (g) determining whether prostate cancer has metastaaized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (i) is also useful as a pharmacodyanamic or pharmacogenomic marker
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                                                                                                                                                                                                                                                                                                                                             Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.
                                                                 Gaps
                                                                 0
 0 U; 9 Other;
                                  Length 2647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2647 BP; 942 A; 475 C; 384 G; 837 T; 0 U; 9 Other;
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28;
                                                                 Indels
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                              0.7%; Score 25; DB 5;
100.0%; Pred. No. 28;
ative 0; Mismatches (
Sequence 2647 BP; 942 A; 475 C; 384 G; 837 T;
                                                                                                                                                                                                                                                                                                                Human prostate expression marker cDNA 25440.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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Pred. No.
                                                                                               3802 ATGTCAAAAAAAAAAAAAAAAAA 3826
                                                                                                                                ATGTCAAAAAAAAAAAAAAAAAAA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Monahan JE;
                                                                                                                                                                                                                BP
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2000US-0207454P.
2000US-0211314P.
2000US-0219007P.
                                                                                                                                                                                                               ABV25449 standard; cDNA; 2647
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                                                               Conservative
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                              Query Match
Best Local Similarity
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Best Local Similarity
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                                                               25;
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                                                             Matches
                                                                                                                                                                                RESULT 10
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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specificaction or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a therapy for inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate call carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indeclace of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker
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                                                                                                                  cytostatic; carcinogen; pharmacodyanamic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                   Human prostate expression marker cDNA 30155.
                                                                                                                                                                                                                                                                                                                                                                                                                      (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 ATGTCAAAAAAAAAAAAAAAAAA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 6531; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monahan JE;
                                                                                                                                  pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABV25571 standard; cDNA; 2647
                                                                                                                                                                                                                                                                                                                  16-MAR-2000; 2000US-0189862P.
25-MAR-2000; 2000US-0207454P.
9-UJW-2000; 2000US-0211314P.
18-JUL-2000; 2000US-0210314P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Endege WO,
                                                                                                                  Human; prostate cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-662795/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                  WO200160860-A2.
                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                    17-FEB-2000;
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                                                                                                                                                                                                                                   23-AUG-2001
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ID ABV2
XX
AC ABV2
XX
DT 16-S
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Gaps

. 0

Indels

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0; Mismatches

100.0%;

25; Conservative

Matches

3802 ATGTCAAAAAAAAAAAAAAAAA 3826

58 ATGTCAAAAAAAAAAAAAAAAA 34

marker; gene; ss

Human; prostate pharmacogenomic

Human prostate

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a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (1) is useful for: (a) assessing whether progression of prostate cancer; (b) monitoring the efficacy of a test compound to inhibit prostate cancer in a patient; (c) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate calculation a patient; (d) assessing the prostate calculation of a compound; (d) determining whether prostate cancer has metastasized in a patient; (h)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                assessing the aggressiveness or indolence of prostate cancer in a patient; (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid molecule (I) comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal sequence trap method; SST method; immunisation; inhibition; infection; allergy; cancer; regulation; tissue formation; tissue repair; activity inhibin activity; chemokine activity; cytokine activity; cytokine activity; metapolic disorder; hormonal disorder; immune disorder; severe combined immunodeficiency; SCID; AIDS; thrombosis; cancer; wound;
                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA encoding a protein identified by the signal sequence trap method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2647 BP; 942 A; 475 C; 384 G; 837 T; 0 U; 9 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 5; Length 2647;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28;
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                                                                                                                                                                                                                                                                    (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 6196-6197; 11750pp; English
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                                                                                                                                                                                                                                                                                                              Monahan JE;
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                                                                                                       2000US-0183319P.
2000US-0189862P.
2000US-0207454P.
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2000US-0219007P.
                                                               2001WO-US005171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
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                                                               20-FEB-2001;
                                                                                                                                                                             09-JUN-2000;
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                                                                                                                                 16-MAR-2000;
25-MAY-2000;
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                       23-AUG-2001
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                                                                 cancer; cytostatic; carcinogen; pharmacodyanamic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
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                     expression marker cDNA 25562.
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Claim 1; Page 5100; 11750pp; English.

Monahan JE

Endege WO,

Schlegel R,

WPI; 2001-662795/76

2000US-0189862P. 2000US-0207454P. 2000US-0211314P.

25-MAY-2000; 09-JUN-2000;

17-FEB-2000; L6-MAR-2000;

20-FEB-2001; 2001WO-US005171

WO200160860-A2

23-AUG-2001

Homo sapiens

13-DEC-2000; 2000US-0255281P

3802 ATGTCAAAAAAAAAAAAAAA 3826

à

Best Local Similarity 100. Matches 25; Conservative

Query Match

ATGTCAAAAAAAAAAAAAAAAAA 34

28

ABV29143 standard; cDNA; 2647

RESULT 13

(first entry)

16-SEP-2002

ABV29143;

WO200160860-A2

Homo sapiens.

0.7%; Score 25;

Ö,

Gaps

0;

```
AAX35694-X35747 represent cDNA sequences that encode novel polypeptides (AAY02358-84) which are identified from a human placental cDNA library by the signal sequence trap (SST) method. The polypeptides have a broad range of physiological activity, including immunisation against and inhibition of infections, allergies and cancer; regulation of tissue formation and repair; activi/inhibin activity; chemokine/cytokine activity; blood coagulation regulation, and receptor/ligand agonist or antagonist activity. The polypeptides can be used for prevention and treatment of disorders including infections by bacteria, years and viruses (including HIV) and protozoa, metabolic and hormonal disorders; immune disorders (including severe combined immunodeficiency (SCID) and
                                                                                                                                                                                                                Polypeptides identified by the signal sequence trap method from a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2796 BP; 636 A; 690 C; 674 G; 796 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AIDS; thrombosis; cancer; and traumatic or surgical wounds
                                                                                                                                                                                                                                                                          Claim 4; Page 153-157; 281pp; Japanese.
                                                                                                         Tada H;
                      97JP-00274674
                                                                                                    Fukushima D, Shibayama S,
                                                            (ONOY ) ONO PHARM CO LTD
                                                                                                                                                 WPI; 1999-277254/23.
                                                                                                                                                                     P-PSDB; AAY02374
                    07-OCT-1997;
                                                                                                                                                                                                                                      CDNA library
```

Query Match 0.7%; Score 25; DB 2; Length 2796; Best Local Similarity 100.0%; Pred. No. 28; Matches 25; Conservative 0; Mismatches 0; Indels 3802 ATGTCAAAAAAAAAAAAAAAAAAA 3826 2768 Argichahahahahahahaha 2792 g

·;

Gaps

· 0

ADD69641 standard; cDNA; 3858 15-JAN-2004 ADD69641; RESULT 15 ADD69641 

Human REMAP cDNA - SEQ ID 70 (first entry)

antiarteriosclerotic; anticonvulsant; nootropic; neuroprotective; cerebroprotective; anti-HIV; antiallergic; antiinflammatory; thyromimetic; cell proliferative; cancer; atherosclerosis; neurological; epilepsy; Huntington's disease; stroke; immune; inflammatory; AIDS; allergy; developmental; hypothyroidism; Cushing's syndrome; infection; human; receptor and membrane-associated protein; REMAP; cytostatic; ss; gene.

Homo sapiens.

WO2003048305-A2.

12-JUN-2003

13-NOV-2002; 2002WO-US036759

2001US-0333097P. 2001US-0340542P. 2001US-034266P. 2001US-0342166P. 2002US-0347580P. 2002US-0348687P. 13-NOV-2001; 15-NOV-2001; 14-DEC-2001; 18-DEC-2001; 1-JAN-2002;

(INCY-) INCYTE GENOMICS INC.

14-JAN-2002;

0 New human receptors and membrane-associated proteins (REWAP), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant REWAP expression e.g. cancer, AIDS, atherosclerosis, or The invention relates to a novel isolated polypeptide comprising a human receptor and membrane-associated protein (REMAP). The polypeptide of the invention demonstrates extostatic, antiatrerisoflarotic, antiatornulsant, nootropic, neuroprotective, cerebroprotective, antiallergic, antiinflammatory and thyromimetic activities and may be useful for treating and diagnosing various disorders including those which are cell proliferative such as cancer and atheroscierosis, neurological including epilepsy, Huntington's disease and stroke, immune/inflammatory particularly AIDS and allergies and developmental such as hypothyroidism Duggan BM, Yang J, Gietzen KJ, Lee SY, Tang YT, Azimzai Y;
Achawla NK, Warren BA, Barroso I, Becha SD, Yue H, Lehr-Mason PM;
Thangavelu K, Lee S, Emerling BM, Kable AE, Khare R, Baughn MR;
Gandhi AR, Tran UK, Richardson TW, Marquis JP, Lal PG, Forsythe IJ;
Hae BA, Swarnakar A, Kallick DA, Griffin JA, Biliott VS, Gorvad AE;
Hafalia AJA, Ison CH, Jin P, Jiang X, Jackson AA, Bhatia U;
Burrill JD, Blake JJ, Ho A, Zheng W, Gao J; and Cushing's syndrome, as well as infections. The current sequence is that of the human REMAP CDNA of the invention. Gaps ·. Score 25; DB 9; Length 3858; Sequence 3858 BP; 972 A; 961 C; 989 G; 936 T; 0 U; 0 Other; 0; Indels 100.0%; Prec. ... 3802 ATGTCAAAAAAAAAAAAAAAA 3826 Claim 5; SEQ ID NO 70; 298pp; English 0.7%; 25; Conservative WPI; 2003-513744/48. Local Similarity P-PSDB; ADD69594 infections Query Match 

3815 ATGTCAAAAAAAAAAAAAAA 3839 ð

completed: September 4, 2004, 08:48:49 Search completed: So Job time: 950 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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sw model OM nucleic - nucleic search, using September 4, 2004, 08:25:37; Search time 183 Seconds (without alignments) 11602.416 Million cell updates/sec Run on:

US-09-927-091-3 3826 Title: Perfect score:

1 aggottgogotggacogaago.....aaaaaaaaaaaaaaaaaaaaa 3826 Sequence:

OLIGO\_NUC Gapop\_60.0 , Gapext 60.0 Scoring table:

682709 seqs, 277475446 residues Searched:

18 Word size :

1852 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 2500 Maximum DB seq length: 5000

Post-processing: Listing first 45 summaries

Database :

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/cgn2 6/ptodata/2/ina/6A\_COMB.seq:\*
/cgn2 6/ptodata/2/ina/PCTUS\_COMB.seq:\*
/cgn2 6/ptodata/2/ina/PCTUS\_COMB.seq:\* Issued Patents NA:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	-09-539-333D-222 Sequence 222,	-09-112-096-28	-08-381-691-16 Sequence 16,	1, 1	US-09-705-299-10 Sequence 10, Appl	'n	Ŋ	-5 Sequence 5,	1,	Ļ	-09-336-643A-82 Sequence 82,	7,	-992-1 Sequence 1,	. ب	3-351-1 Sequence 1,	Sequence 1,	-09-785-381-2 Sequence 2,	-08-986-485-1 Sequence 1,	-09-187-330-2 Sequence 2,	-09-229-583A-1 Sequence 1,	-10-187-904-1 Sequence 1,	-09-518-046-3	-08-960-022-15 Sequence 15,	-08-993-260-4 Sequence 4,	-09-716-129-25 Sequence 25,	-09-716-129-47 Sequence 47,	•
	a ID	SD T	SO E	2 US	4 US	4 US	30	I US	5 PC	JO T	₹ UE	T US	T OF	T C	ži di	3 U.S	30 05	4 US	3 US	4 US	4 US	4 US	3 US	2 US	3 US	4 US	4 US	
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		100	84	3952	75	292	3238	3238	3238	3268	3268	3300	3377	3377	344]	3946	3946	4113	484	487	252	252	2544	255	256	257	258	
οķο	Query	0.6	9.0	9.0	9.0	9.0	•		9.0	9.0	9.0	9.0	9.0	9.0	0.6	9.0		9.0	•	9.0	•		9.0	•	9.0	9.0	9.0	
	Score	24	24	24	23	23	23	23	23	23	23	23	23	23	23	23	53	23	23	23	22	22	22	22	22	22	22	
	Result No.	1	7	c	4	5	9	7	80	σ	10	11	12	13	14	15	J.6	17	18	19	20	21	22	23	24	25	56	
	e	l I		Ų		O																						

Sequence 3, Appli	Sequence 191, App	Sequence 156, App	Sequence 48, Appl	Sequence 48, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 14, Appl	Sequence 26, Appl	Sequence 52, Appl	Sequence 1, Appli	Sequence 26, Appl	~	Sequence 52, Appl		Sequence 191, App
US-09-234-827B-3	US-09-495-050A-191	US-09-370-838-156	US-09-608-285A-48	US-09-557-800C-48	US-09-667-135-1	US-07-938-782A-1	US-08-630-524-1	PCT-US93-08131-1	US-09-636-791A-14	US-09-608-285A-26	US-09-608-285A-52	US-09-240-639-1	US-09-370-265-26	US-09-557-800C-26	US-09-557-800C-52	US-09-370-625A-26	US-09-149-476-191
4	4	4	4	4	4	Н	Н	Ŋ	4	4	4	4	4	4	4	4	4
2606	2657	2668	2693	2693	2718	2729	2729	2729	2752	2762	2762	2762	2762	2762	2762	2762	2779
9.0	9.0	9.0	9.0	9.0	9.0	9.0	9.0	9.0	9.0	9.0	9.0	9.0	9.0	9.0	9.0	9.0	9.0
22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22
88	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

```
OTHER INFORMATION: 99-27349-267 : polymorphic base G or A
                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc binding
LOCATION: 1502_.1521
OTHER INFORMATION: 99-27349-267.mis1, complement
       Sequence 222, Application US/09539333D Patent No. 6476208
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, 11ya
                                                                   Bougueleret, Lydie
Bihain, Bernard
                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: misc_binding
LOCATION: 1482..1500
                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: allele
LOCATION: 1501
US-09-539-333D-222
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Gaps

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Indels

Length 3952;

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GENERAL INFORMATION:
APPLICANT: Lex M. Cowsert
APPLICANT: Lex M. Cowsert
APPLICANT: Susan M. Preier
TITLE OF INVENUENCE RTS-0174
FILE REFERENCE: RTS-0174
CURRENT PAPLICATION UNBER: US/09/705,299
CURRENT FILING DATE: 2000-11-01
NUMBER OF SEQ ID NOS: 86
LENGTH: 2929
TYPE: DNA
TYPE: DNA
TYPE: DNA
CORANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
LOCATION: (70)...(1581)
OTHER INFORMATION: Human CYP3A4 CDNA reference sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lichter, Jay
APPLICANT: Guido, Marco
TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
FILE REFERRNCE: SEQ-12P
CURRENT APPLICATION NUMBER: US/09/144,367
CURRENT APPLICATION NUMBER: 60/058,612
PRIOR FILING DATE: 1998-08-31
PRIOR FILING DATE: 1997-09-10
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FASLSEQ for Windows Version 3.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4;
                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                     0.91;
                                                                                                                                                                                                                                                                                                             Query Match 0.6%; Score 24; DB Best Local Similarity 100.0%; Pred. No. 0.9 Matches 24; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 0.6%; Score 23; DB Best Local Similarity 100.0%; Pred. No. 2.5 Matches 23; Conservative 0; Mismatches
CURRENT APPLICATION DATA:

APPLICATION WUMBER: US/08/381,691
INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 3952 base pairs

TYPE: nucleic acid
STRANDENNESS: double
STRANDENNESS: double
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                         3803 TGTCAAAAAAAAAAAAAA 3826
                                                                                                                                                                                                                                                                                                                                                                                                                                                     3856 TGTCAAAAAAAAAAAAAAAA 3833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3804 GTCAAAAAAAAAAAAAAAAA 3826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10, Application US/09705299 Patent No. 6440737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09144367 Patent No. 6432639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: H. sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-705-299-10/c
                                                                                                                                                                                                                                           , ANTI-SENSE:
US-08-381-691-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-144-367-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 4
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                                                  NAME/KEY: primer bind
LOCATION: 1748...767
OTHER INFORMATION: upstream amplification primer, complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 0.6%; Score 24; DB 4; Length 3001; Best Local Similarity 100.0%; Pred. No. 0.92; Matches 24; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 24; DB 3; Length 3848;
Pred. No. 0.91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Melhel H. Shapero
APPLICANT: Michael H. Shapero
APPLICANT: Larisa Tsavaler
TITLE OF INVENTION: Prostate Tumor Polynucleotide and
TITLE OF INVENTION: Antigen Compositions
FILE REFERENCE: 7636-0015.30
CURRENT APPLICATION NUMBER: US/09/112,096
CURRENT FILING DATE: 1998-07-09
EARLIER APPLICATION NUMBER: 60/056,110
EARLIER APPLICATION NUMBER: 60/056,110
MUMBER OF SEQ ID NOS: 29
SOFTWARE: FRANCE FRANCE 1997-08-20
SOFTWARE: FRANCE FOR WINDOWS Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
TITLE OF INVENTION: Alpha-lac Albumin Gene Constructs
NUMBER OF SEQUENCES: 17
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                  LOCATION: 1337.1355
OTHER INFORMATION: downstream amplification primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3803 TGTCAAAAAAAAAAAAAAAAA 3826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3803 TGTCAAAAAAAAAAAAAAAAAA 3826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2367 TGTCAAAAAAAAAAAAAAAAA 2390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3780 TGTCAAAAAAAAAAAAAAAAA 3803
                                                                                                                                                                                                                                                              LOCATION: 1489.1513 COTHER INFORMATION: 99-27349-267 probe
       INFORMATION: 99-27349-267.mis2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 28, Application US/09112096
Patent No. 6194152
GENERAL INFORMATION:
APPLICANT: Reiner Laus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.6%; SCUL
100.0%; Pre
0; '
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; Sequence 16. Application US/08381691
Patent No. 5852224
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
1 LOCATION: 182,848,1501,2206,2397
2 CTHER INFORMATION: n=a, g, c or t
US-09-539-333D-222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
US-09-112-096-28
                                                                                                                                                                                                                                         NAME/KEY: misc_binding
                                                                                                                                               NAME/KEY: primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 28
LENGTH: 3848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 2
US-09-112-096-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24;
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Best Local
                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                   FEATURE:
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δ Οp 0

Gaps

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Matches

à g RESULT 3

US-09-705-299-10

Length 2759;

à

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Query Match

0.6%; Score 23; DB 4; Length 3238;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 23; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                              ADDRESSEE: Genetics Institute Inc.- Legal Affairs
STREET: 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMERS: US/09/874,628
FILING DATE: 05-Jun-2001
CLASSIFICATION: <unimage to the company of the company o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application PC/TUS9410080
GENERAL INFORMATION:
APPLICANT: GENETICS INSTITUTE, INC.
TITLE OF INVENTION: RECEPTOR PROTEINS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute Inc.- Legal Affairs
STREET: 87 CambridgePark Drive
CITY: Cambridge
CITY: Cambridge
                               THIES, R. SCOLT YAMAJI, NO. 66105130ru
TITLE OF INVENTION: RECEPTOR PROTEINS NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
RAPLICATION WINBER: 08/123,934
FILING DATE: 17-5EP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 474..2000
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: LAZAR, Steven R
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3804 GTCAAAAAAAAAAAAAAA 3826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3157 GTCAAAAAAAAAAAAAAAAA 3179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 876 1170
TELEFAX: 617 876 5851
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3238 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CELESTE, Anthony J.
                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                ZIP: 02140
COMPUTER READABLE FORM:
                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLONE: CFK1-10a
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                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCT-US94-10080-5
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STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
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                        DB 4; Length 2929; 2.5;
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100.0%; Pred. No. 2.5;
tive 0; Mismatches 0; Indels
                                                                                         0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM:
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,934A
FILING DATE: 17-5EP-1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: LAZAR, Steven R
REGISTRATION NUMBER: 5203
TELEPHONE: 617 876 1170
TELEPHONE: 617 876 5851
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3228 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: WOZNEY, John
APPLICANT: CELESTE, Anthony J.
APPLICANT: THIES, R. Scott.
APPLICANT: THIES, R. Scott.
TITLE OF INVENTION: RECEPTOR PROTEINS
NUMBER OF SEQUENCES: 19
CORRESPONDENCES: 19
ADDRESSEE: Genetics Institute Inc.- Legal Affairs
STREET: 87 CambridgePark Drive
                    0.6%; Score 23; DB ilarity 100.0%; Pred. No. 2.5 Conservative 0; Mismatches
                                                                                                                                                        3802 AIGICAAAAAAAAAAAAA 3824
                                                                                                                                                                                                                      1806 ATGTCAAAAAAAAAAAAAAAA 1784
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Patent No. 6291206
GENERAL INFORMATION:
APPLICANT: WOZNEY, John
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Sequence 5, Application US/09874628
Patent No. 6610513
GENERAL INFORMATION:
APPLICANT: WOZNEY, John
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                        Query Match
Best Local Similarity
Matches 23; Conserv
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Best Local Similarity
Matches 23; Conserv
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CITY: Cambridge
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US-08-123-934A-5
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APPLICANT: Rutter, Marc
APPLICANT: Rutter, Marc
APPLICANT: Rutter, Marc
APPLICANT: Rutter, Marc
TITLE OF INVENTION: No. 6399761el Human Potassium Channels
TITLE OF INVENTION: NO. 6399761el Human Potassium Channels
CURRENT APPLICATION NUMBER: US/09/336,643A
CURRENT APPLICATION NUMBER: 60/076,687
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-01-19
PRIOR FILING DATE: 1999-01-19
PRIOR FILING DATE: 1999-01-19
PRIOR FILING DATE: 1999-02-22
NUMBER: OF SEQ ID NOS: 87
SEQ ID NOS: 87
SEQ ID NO 82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 3300; 2.5;
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.00.0%; Pred. No. 2.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                            APPLICANT: MARTINEZ, RICARDO
APPLICANT: WHYTE, DAVID
TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
FILE REPERRANCE: 038602/0329
CURRENT APPLICATION NUMBER: US/09/291,417D
CURRENT FILING DATE: 1999-04-13
PRIOR FILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 155
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
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Pred. No.
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100.0%; Pre
                Sequence 1, Application US/09291417D Patent No. 680170 GENERAL INFORMATION: APPLICANT: PLOWMAN, GREGORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
US-09-819-989-1
; Sequence 1, Application US/09819989
                                                                                                                                                                                                                                                                                                                                                                                                                              100.08; PEC
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APPLICANT: Miller, Andrew P.
APPLICANT: Curran, Mark Edward
APPLICANT: Hu, Ping
APPLICANT: Rutter, Marc
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Best Local Similarity 100.
Matches 23; Conservative
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; LOCATION: (50)...(1285)
US-09-336-643A-82
                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-09-291-417D-1
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ORGANISM: H. sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                          LENGTH: 3268
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  US-09-291-417D-1
                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09688188B
Factent No. 6656716
GENERAL INFORMATION:
APPLICANT: PLOWDAN, GREGORY
APPLICANT: PLOWDAN, GREGORY
TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
FILE REPRENCE: 038602/0328
CURRENT APPLICATION NUMBER: US/09/688,188B
CURRENT FILING DATE: 1999-04-14
FRIOR APPLICATION NUMBER: 60/081,784
FRIOR FILING DATE: 1999-04-14
FRIOR APPLICATION NUMBER: 60/081,784
FRIOR FILING DATE: 1998-04-14
STOR FILING DATE: 1998-04-14
STOR FILING DATE: 1998-04-14
STOR FILING DATE: 1998-04-14
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10080
                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,934
FILING DATE: 17-SEP-1993
CLASSIFICATION NUMBER: 05.08/123,934
ATTORNEY/AGENT INFORMATION:
NAME: LAZAR, SLEVER REGISTRATION NUMBER: 32.618
REGISTRATION NUMBER: 25.03-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-5851
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LEWGIN 328 BASE PAIRS
STRANDENNES: SINGLE
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MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: CFK1-10a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23; Conservative
                                                             HEREWITH
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474..2000
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                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE SEQ ID NO 1
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NAME/KEY:
LOCATION:
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US-09-688-188B-1
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APPLICANT: Tunas, Daniel

PEPLICANT: Tunas, Daniel

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548PLC1

CURRENT APPLICATION NUMBER: US/09/866,028

CURRENT PILING DATE: 2001-05-25

Prior application data removed - consult PALM or file wrapper

NUMBER OF SEQ ID NOS: 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Sheffield, val C.
APPLICANT: Alward, Mallace L.M.
APPLICANT: Stone, Edwin M.
APPLICANT: Stone, Edwin M.
APPLICANT: Nishimura, Darryl
APPLICANT: Datall, Shiva
TITLE OF INVENTION: THEAPBUTICS AND DIAGNOSTICS FOR
TITLE OF INVENTION: TRANSCRIPTION FACTOR
TITLE OF INVENTION: TRANSCRIPTION FACTOR
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                         Query Match 0.6%; Score 23; DB 4; Length 3441; Best Local Similarity 100.0%; Pred. No. 2.5; Matches 23; Conservative 0; Mismatches 0; Indels
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ZIP: 02109-2170
COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/083,351
FILING DATE: 22-MAY-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: ATTORNEY/AGENT INFORMATION:
NAME: ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 35.430
REFERENCE/DOCKET NUMBER: UIA-029.02
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STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 1, Application US/09083351; Patent No. 6087107; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 3946 base pairs
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STRANDEDNESS: single
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475..2133
                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo Sapien
US-09-866-028-6
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MOLECULE TYPE:
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, LOCATION:
US-09-083-351-1
                                                                                                                                                                                                                              SEQ ID NO 6
LENGTH: 3441
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                                                                                                                                                                                                                                                                                TYPE: DNA
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GENERAL INFORMATION:
APPLICANT: WEI, Ming-Hui et al.
TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
TITLE OF INVENTION: THEREOF PROFESSOR FILE REFERENCE: CLOO1200
CURRENT FILING APPLICATION NUMBER: US/09/819,989
CURRENT FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INCORMATION:
APPLICANT: WEI, Ming-Hui et al.
TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID HUMAN ENZYME PROTEINS, AND USES
TITLE OF INVENTION: THEREN BOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
TITLE OF INVENTION: THEREN BOLECULES
TITLE OF INVENTION: THEREN INVENTION: THEREN INVENTION: THEREN INVENTION NUMBER: US/10/273,992
CURRENT FILING DATE: 2002-10-21
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
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100.0%; Pred. No. 2.5;
ative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1 LENGTH: 3377
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Patent No. 6664093
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Patent No. 6642360
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Grimaldi, Christopher
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Filvaroff, Ellen
Gerritsen, Mary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23; Conservative
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APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
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Napier, Mary
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Matches 23; Conserv
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ORGANISM: Human
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; ORGANISM: Human
US-10-273-992-1
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Search completed: September 4, 2004, 13:14:42 Job time : 185 secs

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4, 2004, 08:32:53; Search time 1152 Seconds (without alignments) 16508.391 Million cell updates/sec
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cgn2_6/prodata/2/pubpna/US07_NEW_PUB.seq:*

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cgn2_6/prodata/2/pubpna/US06_PUBCOMB.seq:*

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cgn2_6/prodata/2/pubpna/US09_NEW_PUB.seq:*

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cgn2_6/prodata/2/pubpna/US09_PUBCOMB.seq:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3267054 seqs, 2485319735 residues
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Perfect score:
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	Description	Sequence 3, Appli	Sequence 141, App	Sequence 1164, Ap	Sequence 100661,	Sequence 39, Appl	Sequence 875, App	Sequence 1916, Ap	Sequence 51, Appl	Sequence 51, Appl	Sequence 137631,	Sequence 11, Appl	Sequence 54840, A	Sequence 12, Appl	Sequence 108. App
SUMMARIES	D	US-09-927-091-3	US-10-295-027-141	US-10-295-027-1164	US-10-437-963-100661	US-09-745-763-39	US-10-104-047-875	US-10-106-698-1916	US-09-529-063-51	US-10-414-378-51	US-10-424-599-137631	US-10-615-659-11	US-10-437-963-54840	US-10-615-659-12	US-10-450-826-108
	DB	6	16	16	17	6	16	15	σ	15	13	17	17	17	17
	% Query Match Length DB	3826	4702	4702	2511	2522	2586	2629	2796	2796	2806	3465	3504	3554	4572
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 3826; Conservative 0; Mismatches

TYPE: DNA ORGANISM: Human

US-09-927-091-3

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1 AGCTGCGCTGGACCGAAGCGCTGCTGCTAAGCTCGCGGGGGTAAGGGGTCGCCTGGG 61 CCAGGGTTTGGGGCCGGGATCCCGGCAGCTGAGCGGGCCGGCACCCCTCCTTCTCTGCC

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15	25	0.7	4740	6	US-09-945-265-3	Segmence 3. Appli
16	25	0.7	4740	10	S-09-902-481A-	2
17	25	0.7	4740	15	US-10-207-655-175	Semience 175. App
18	25		4740	1,5	-10-136-819-18	Semience 18, April
61	25		4740	1 -	-10-159-563-3	Semience 339 Ann
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210	1 6	9 4	2602	1	7-10-636-63-63-1	Sequence 340, App
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C 24	24		2645	14	US-10-044-090-799	Sequence 799, App
57	47		T997	T-P	-159-563-39	395
26	24		2661	17	US-10-211-179-4	4
27	24		2677		S-09-733-643-1	Sequence 1, Appli
28	24		2840		US-09-978-295A-611	611,
29	24		2840		US-09-978-697-611	611,
30	24		2840	σ	US-09-978-192A-611	611,
31	24		2840	σ	US-09-999-832A-611	611,
32	24		2840	10	US-09-978-189-611	e 611
33	24		2840	10	US-09-978-608A-611	e 611
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38	24		2840	10	US-09-999-833A-611	
39	24	٠.	2840	10	US-09-981-915A-611	611,
40	24		2840	10	US-09-978-824-611	611,
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44	4 C		t a	9 0	9-VCET-0/6-60-	611
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RESULT 1						
US-09-927-091-3	7-091-3					
; Seguence	'n	plicat	Application US/09927091	0992	7091	
; Patent No.	No. US2	002011	9541A1			
; GENERAI	GENERAL INFORMATION	ATION:				
; APPLICANT	ANT: KI		ANN			
, APPLICANT:		LOTT, S'	STEVE			
, APPLICANT	ANT: C	HANDLE	CHANDLER, DAWN			
TITLE ;	TITLE OF INVENTION: THE TUMOR	NOLLN	THE TO		SUPPRESSOR CAR-1	
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APPLICANT: Watson, Susan R.
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
FILE REFERENCE: 0.18501-0.12500US
CURRENT APPLICATION NUMBER: US/10/295,027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 1386
SOFTWARE: Patentin Ver. 2.1
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100.0%; Pred. No. 0.049;
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100.0%; Pred. No. 0.049;
tive 0; Mismatches 0.
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PRIOR PELICATION NUMBER: US 09/663,733
PRIOR PELING DATE: 2000-09-15
PRIOR PLING DATE: 2000-15
PRIOR PLING DATE: 2000-11-13
PRIOR PELING DATE: 2001-11-15
PRIOR PELING DATE: 2001-11-15
PRIOR PELING DATE: 2001-11-21
PRIOR PELING DATE: 2001-11-21
PRIOR PELING DATE: 2001-11-21
PRIOR PELING DATE: 2001-11-29
PRIOR PELING DATE: 2001-11-29
PRIOR PELING DATE: 2001-11-29
PRIOR PELING DATE: 2001-12-14
PRIOR PELING DATE: 2001-12-14
PRIOR PELING DATE: 2001-12-14
PRIOR PELING DATE: 2002-01-08
PRIOR PELING DATE: 2002-01-08
PRIOR PELING DATE: 2002-01-08
PRIOR PELING DATE: 2002-01-10
PRIOR PELING DATE: 2002-02-03
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Publication No. US20030232350A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2002-11-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Afar, Daniel
APPLICANT: Afar, Daniel
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kurt C.
APPLICANT: Gish, Kurt C.
APPLICANT: Gish, Kurt C.
APPLICANT: Hevezi, Peter A.
APPLICANT: Mack, David H.
                                                                                                                                                                  26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 26; Conservative
; LENGTH: 4702
; TYPE: DNA
; ORGANISM; Homo sapiens
US-10-295-027-141
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                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE:
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US-10-295-027-1164
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RESULT 4

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APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 100661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 17; Length 2511; 0.16;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO Compartible
COMPUTER: TBM FO Compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/745,763
FILING DATE: 18-Jun-2000
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , OTHER INFORMATION: Clone ID: PAT_MRT4530_98356C.1
US-10-437-963-100661
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100.0%; Pred. No. 0.1
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute,
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3802 ATGTCAAAAAAAAAAAAAAAAAAAAA 3826
Sequence 100661, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            McCoy, John M.
LaVallie, Edward R.
Collins-Racie, Lisa A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Sprunger, Suzanne A.
REGISTRATION WUMBER: 41,323
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284
TELEPHONE: (617) 876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 ATGTCAAAAAAAAAAAAAAAAA
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Patent No. US20020065394A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Merberg, David
Treacy, Maurice
Spaulding, Vikki
TITLE OF INVENTION: SECRETED
ENCODING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Jacobs, Kenneth
                                                                                                                                                                                       Boukharov, Andrey A.
                                                                  APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Cambridge
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                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-745-763-39
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Sequence 51, Application US/09529063

Sequence 51, Application US/09529063

Sequence 51, Application US/09529063

Sequence 51, Application US/09529063

Sequence 51, Application Sequence 51, Application Sequence 51, Application Sequence 51, Application Sequence 51, Applicant 
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Publication No. US20030165981A1
GENERAL INFORMATION:
APPLICANT: FUKUSHIMA, DAIKICHI
APPLICANT: FUKUSHIMA, SHIRO
TITLE OF INVENTION: FOLYPEPTIDE, CDNA ENCODING THE POLYPEPTIDE, AND USE OF
                                                                                                                                                                               Gaps
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Pred. No. 0.16;
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100.0%; Pred. No. 0.16;
Live 0; Mismatches 0; Indels
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                                                                                                                                                                         0;
                                                                                         0.7%; Sco...
100.0%; Pred. No. ...
0; Mismatches
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CURRENT FILING DATE: 2003-04-16
PRIOR APPLICATION NUMBER: US/09/529,063
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 1998-10-06
PRIOR APPLICATION NUMBER: PCT/JD98/04514
PRIOR FILING DATE: 1998-10-06
PRIOR APPLICATION NUMBER: UP 9-274674
PRIOR FILING DATE: 1997-10-07
NUMBER OF SEQ ID NOS: 117
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                  ; OTHER INFORMATION: n equals a,t,g, or c
US-10-106-698-1916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3802 ATGTCAAAAAAAAAAAAAAAAA 3826
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FATION: (11)..(58)
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NAME/KEY: mat peptide
LOCATION: (59)...(1273)
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (11)..(1273)
                                                                                                     Query Match
Best Local Similarity
Matches 25; Conserve
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Matches 25; Conserv
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Publication No. US20030109690A1
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US/10/106,698
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-11-03
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8664
SEQ ID NO 1916
LENGTH: 2629
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Fublication No. US20030236392A1
GENERAL INFORMATION:
TITLE OF INVENTION: No. US20030236392A1e1
FILE REPERENCE: H1-A0105
CURRENT APPLICATION NUMBER:
PRIOR PELLING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE PLANCE PATENTION: VET. 2.1
SEQ ID NO 875
LENGTH: 2586
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                                                                                         TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear MOLECULE TYPE: cDNA SEQUENCE DESCRIPTION: SEQ ID NO: 39: US-09-745-763-39
                                                                                                                                                                                                                                                                                                                                                                                                                         3802 ATGTCAAAAAAAAAAAAAAAAAAAA 3826
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INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 2522 base pairs
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US-10-104-047-875
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: misc feature
LOCATION: (35)...(35)
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US-10-104-047-875/c
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APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
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Sequence 12, Application US/10615659

Sequence 12, Application US/10615659

Publication No. US2004015723431

GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN

TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42

FILE REFERENCE: D0283 NP

CURRENT APPLICATION NUMBER: US/10/615,659

CURRENT FILING DATE: 2003-07-09

PRIOR PRILING DATE: 2003-07-09

PRIOR FILING DATE: 2002-07-09
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100.0%; Pred. No. 0.16;
                                                                                                         Score 25; DB 17; Length 3465; Pred. No. 0.16;
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// CTHER INFORMATION: Clone ID: PAT_MRT4530_56905C.1
US-10-437-963-54840
                                                                                                 0.7%; Sco...
100.0%; Pred. No. v...
0; Mismatches
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Pred. No.
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                                                                                                                                                                                                                                                         3441 ATGTCAAAAAAAAAAAAAAAAAAAAAAA 3465
                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 54840, Application US/10437963; Publication No. US20040123343A1
                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: AROSA, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
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100.0%;
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SOFTWARE: Patentin version 3.2
SEQ ID NO: 3554
LENGTH: 3554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 25; Conservative
                                                                                                                Query Match
Best Local Similarity 100.0
Matches 25; Conservative
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CRGANISM: Homo sapiens
US-10-615-659-12
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ORGANISM: Oryza Bativa
                     TYPE: DNA
CORGANISM: Homo sapiens
US-10-615-659-11
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Best Local Similarity
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LENGTH: 3465
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Sequence 137631, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Coo Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 1942163318
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF ESO ID NOS: 285684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11, Application US/10615659
; Publication No. US20040157234A1
; GENERAL INFORMATION:
; APPLICAMT: BILSTOL-Wers Squibb Company
; TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42
; TILLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42
; TILLE TERFERENCE: DO283 NP
; CURRENT APPLICATION NUMBER: US/10/615,659
; CURRENT FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: U.S. 60/394,725
; PRIOR APPLICATION NUMBER: U.S. 60/394,725
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0.7%; Score 25; DB 13; Length 2806;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 25; Conservative 0; Mismatches 0; Indels
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0.7%; Score 25; DB 15; Length 2796;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 25; Conservative 0; Mismatches 0; Indels
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SOFTWARE: Patentin Version 3.2
SEQ ID NO 11
         SOFTWARE: Patentin Ver. 2.1
                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                        ; NAME/KEY: CDS
; LOCATION: (11)..(1273)
US-10-414-378-51
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NAME/KEY: sig_peptide
LOCATION: (11)..(58)
                                                                                                                                                                                                                    NAME/KEY: mat peptide LOCATION: (59)..(1273)
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LENGTH: 2806
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US-10-615-659-11
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                                    SEQ ID NO 51
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Search completed: September 4, 2004, 13:34:15 Job time: 1155 secs
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Publication No. US20040101818A1

GENERAL INFORMATION:

APPLICANT: Axalrad, Douglas W.

APPLICANT: Cook, Jonathon S.

APPLICANT: Daiswal, Neelam

APPLICANT: Bisteln, Richard

APPLICANT: Bisteln, Richard

APPLICANT: Houghton, Adam

APPLICANT: Bisteln, Richard

APPLICAN
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Patent No. US20020125614A1

GENERAL INFORMATION:

APPLICANT: Springer, Timothy A.

APPLICANT: Springer, Timothy A.

APPLICANT: IJ, Chafen

TITLE OF INVENTION: MODIFIED POLYPEPTIDES STABILIZED IN A.

TITLE OF INVENTION: DESTRED CONFORMATION AND METHODS FOR PRODUCING SAME

TITLE OF INVENTION: UNMBER: US/09/945,265

CURRENT FILING DATE: 2001-08-31

PRIOR APPLICATION NUMBER: US 60/229,700

PRIOR APPLICATION NUMBER: US 60/229,700

NUMBER OF SEQ ID NOS: 4

SOFFWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 3
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0.7%; Score 25; DB 9; Length 4740;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 25; Conservative 0; Mismatches 0; Indels
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US-10-450-826-108
    0; Mismatches
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    Conservative
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ORGANISM: Homo sapiens
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CRGANISM: Homo sapiens
US-09-945-265-3
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Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:C230023D16 product:similar to CDNA FLJ10759 FIS. CLONE NT2RP5004617, WRAKLY SIMILAR TO ZINC-BINDING PROTEIN A33 [Homo sapiens], full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Idjh-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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PUBMED REFERENCE AUTHORS 20530913 11076861

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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 81 Row: p Column: 13
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, GenomeScan gene prediction
This clone has the following problem: retained intron.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: nisc_groenhari.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupca,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                             Craniata, Vertebrata, Euteleostomi,
Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                             652 ATCTACCAGGACCCGGTGAGCCTGGGCTGCGAGCACTACTTCTGCCGCCGCTGCATCAC 710
                                                                                                                                                                                                                                                                                                                    540 ATCTACCAGGACCCGGTGAGCCTGGGGAGCACTACTTCTGCCGCCGCTGCATCAC 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (13-SB2-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                      592 GCCCCTGGCGCCATGGCGTGCAGCTCAAGGACGAGCTGCTGTGCTCCATCTGCCTGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
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/clone lib="NIH MGC_94"
/lab_host="DH10B"
   Length 2726;
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Contact: MGC help desk
3.1%; Score 119; DB 11;
100.0%; Pred. No. 3.6e-14;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA
mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BC037619 3080 bp
Mus musculus, clone IMAGE:5400144,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="IMAGE:5400144"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Rodentia,
1 (bases 1 to 3080)
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Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BC037619.1 GI:22902286
                                       Best Local Similarity 100.
Matches 119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg, R.
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les 25; Conserv
       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
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JOURNAL
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Matches
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BC037619
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
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                                                 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Komo, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Murametsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. sequencing pipeline with 384 multicapillary sequencer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:genome-res@gec.riken.go.jp, Pax:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="cerebellum"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="0 day neonate"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The RIKEN Genome Exploration Research Group Phase II Team and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA library was prepared and sequenced in Mouse Genome broyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The FANTOM Consortium and the RIKEN Genome Exploration Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
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/db_xref="MG1:2415428"
/db_xref="taxon:10090"
/clone="c230025D16"
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 420, 563-573 (2002)
6 (bases 1 to 2726)
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FEATURES

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LOCUS

RESULT 3 BC052223 ORGANISM

REFERENCE

ACCESSION VERSION KEYWORDS SOURCE

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Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamanoto, H., Sakayuchi, S., Ikegami, T., Kashiwadi, K., Yoneda, Y., Ishikawa, T., Ozawa, Y., Izawa, M., Ohara, B., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muranatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AKOB5089 2963 bp mRNA linear HTC 20-SEP-2003 Mus musculus 13 days embryo lung cDNA, RIKEN full-length enriched library, clone:D430035B22 product:unclassifiable, full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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clone has the following problem: no cloning site /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.6%; Score 24; DB 11; Length 2779;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                          adult male"
                                                                                                                    | 1.2779, | 2.779, | 2.779, | 2.779, | 2.779, | 2.779, | 2.779, | 2.779, | 2.779, | 2.779, | 2.779, | 2.779, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 2.790, | 
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                                    Location/Qualifiers
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HTC; CAP trapper.
Mus musculus (house mouse)
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                                        microdeletion.
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Best Local Similarity
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LOCUS
                                                                                                                                      source
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PUBMED
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Dukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
I (Dases 1 to 2779)
I (Lases 1 to 2779)
I (Callins, F.S., Wagper, L., Shemmen, C.M., Schuler, G.D., Altschul, S.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninot, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McKernan, R.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Fullyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.B.
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CONTACT: MGC help desk
CONTACT: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Sumio Sugano
CDNA Library Preparation: Dr. Sumio Sugano
CDNA Library Preparation: Dr. Sumio Sugano
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Brin Garland, Ran Guin,
Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
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Submitted (02-MAY-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 104 Row: n Column: 23
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein
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                                                                                                                                                                                                                                                                                                                                                       linear
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Danio rerio cDNA clone IMAGE:5915784.
BC052223
                                                          3802 ATGTCAAAAAAAAAAAAAAAAA 3826
                                                                                                                                              3003 ATGTCAAAAAAAAAAAAAAAAAAA 3027
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AUTHORS JOURNAL

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S. Adachi, J., Aizawa, Y., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Rukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayatsu, N., Hiramcto, K., Hiraoka, T., Hirozane, T., Haroi, F., Ishi, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Nakamura, M., Noshi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saitoh, R., Saitoh, H., Sakai, C., Sakai, K., Sakaume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Takaku, Tagami, M., Tagawa, A., Takahashi, F., Takaku, Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
                                                                      Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itôh, M., Konno, H., Oƙazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                  Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. sequencing pipeline with 384 multicapillary sequencer General Connec Res. 10 (11), 1757-1771 (2000)
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/clone="8931054008"
/tissue type="cerebellum"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3234)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The RIKEN Genome Exploration Research Group Phase II Team and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 409, 685-690 (2001)
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S Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Pukuda, S., Furuno, M., Hangaki, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hiramoto, K., Hiraoka, T., Hirozane, T., Hayashida, K., Hayatsu, M., Hiramoto, K., Hiraoka, T., Hirozane, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, M., Kagawa, T., Kawai, J., Kojima, Y., Kondo, S., Komno, H., Kouda, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazi, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shizaki, T., Sakazume, N., Sogabe, Y., Tanaka, T., Tomaru, A., Takahashi, F., Takaku-Akahira, S., Muramarsu, M. and Hayashizaki, Y. Takahashi, F., Takaku-Akahira, S., Direct Submission Hayashizaki, Y.

Direct Submission Hayashizaki, Y.
Direct Submission Hayashizaki, Y.
Direct Submission Research (Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail;genome-res@gsc.riken.go.jp, Fax:81-45-503-9216)

Fax:81-45-503-9216)
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/dev stage="13 days embryo"
1. .2963
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3234 bp mRNA linear HTC 20-SEP-2003
Mus musculus 10 days neonate cerebellum cDNA, RIKEN full-length
enriched library, clone:B930054008 product:unclassifiable, full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Please visit our web site for further details.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="FANTOM_DB:D430035E22"
/db_xref="MGI:2421960"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.6%; Score 24; DB 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
/clone="D430035E22"
/tissue_type="lung"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="unclassifiable"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 TGTCAAAAAAAAAAAAAAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/strain="C57BL/6J"
   Nature 420, 563-573 (2002)
6 (bases 1 to 2963)
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HTC; CAP trapper.
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Best Local Similarity
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AK081017
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DEFINITION
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JOURNAL
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TITLE
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MEDLINE
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                                   REFERENCE
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SOURCE
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/clone="K58"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0
Matches 24; Conservative
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DEFINITION
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VERSION
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TITLE
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CA916724
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Mus musolus

Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Musolus

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausberg, R.L., Collins, F.S., Magner, L., Shenmen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Magner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.L., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Barmer, A.A., Rubin, G.M., Hong, L.,
Stapleron, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Morsenan, K.J., Malek, J.A., Gunarane, P.H., Richards, S.,
Morlay, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Hellcon, E., Ketteman, M., Madan, A., Roud, A.C., Shevchenko, Y.
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-remail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Gudan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                    HTC 19-NOV-2003
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                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                 BC035530 3250 bp mRNA linear HTC 1:
Mus musculus RIKEN cDNA 1200014D22 gene, mRNA (cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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0
                                                                                                                                 0.6%; Score 24; DB 11; Length 3234; 100.0%; Pred. No. 2.1e+04; tive 0; Mismatches 0; Indels C
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Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA
/dev_stage="10 days neonate"
L. .3234
                                                                                                                                                                                                                                                3803 TGTCAAAAAAAAAAAAAAAAAA 3826
                                                       /note="unclassifiable"
                                                                                                                                                                                                                                                                                                  132 TGTCAAAAAAAAAAAAAAAAA 155
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Mus musculus
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2 (bases 1 to 3250)
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                                                                                                                                                                                           24; Conservative
                                                                                                                                                                   Similarity
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                                 misc_feature
                                                                                                                                          Query Match
Best Local 8
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VERSION
KEYWORDS
SOURCE
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PUBMED
REFERENCE
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JOURNAL
                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
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COMMENT
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BC035530
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRRK plate: 65 Row: e Column: 18 This clone has the following problem: retained intron. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CA016724 14-MAR-2003 X58FL human keratinocyte matchmaker cDNA library Homo sapiens cDNA clone K58 5' similar to Arkadia, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell type="keratinocyte"
/cell_line="HaCat cell line;derived from long term primary
human adult skin keratinocyte"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3415)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scarafia, L.B., Stoufer, S.D. and Swinney, D.C.
Identification of Ring Finger proteins that interact with UbcH5a, an ubiquitin-conjugating enzyme
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: liliana scarafia@roche.com
Full length single stranded sequencing of baited insert
Insert Length: 3000 Std Error: 0.00
Seq primer: primer 2 (5395)TACCACTACAATGGATG;and insert-specific
POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="yeast/S.coli"
/close lib="human keratinocyte matchmaker cDNA library"
/close lib="human keratinocyte matchmaker cDNA library"
/notes="Vector 2: Site 1: EcoNI; Site 2: XhoI;
Matchmaker yeast two-hybrid sytem from clontech; pACT2
vector has GAL4 AD and HA pittope under ADH1 promoter.
This oligo-dT primed library was screened with human UbcH5a as bait, to obtained interacting proteins."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue type="Bye, retina, mouse strain C57Bl\6"
/clone lib="NIH MGC_94"
/lab host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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Tel: 650 354 7997
Fax: 650 354 7554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 24; DB 11; Length 3250; Pred. No. 2.1e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pCMV-SPORT6"
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:5366096"
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CA916724.1 GI:28951961
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/clone="SSA355"
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                    GI:2706770
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Matches 24; Conservative
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This clone was selected for full length sequencing because it passed the following selection criteria: Genomescan gene prediction This clone has the following problem: retained intron.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3444)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (01-NOV-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                      Gaps
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
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                                 Score 24; DB 14; Length 3415; Pred. No. 2e+04;
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100.0%; Pred. No. 2e+04;
tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                   linear
                                                                      0; Indels
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                                                                                                                                                                                                                          3444 bp mRNA Homo sapiens, clone IMAGE:3847010, mRNA. BC039604
                      100.0%; Scc...
100.0%; Pred. No. 2...
... 0; Mismatches
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                                                                                                        TGTCAAAAAAAAAAAAAAAA 3826
                                                                                                                                          3388 TGTCAAAAAAAAAAAAAAAA 3411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                      BC039604.1 GI:25058528
                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
                                                                     Conservative
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Matches
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Straubberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Straubberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Altschul, S.F., Zeeberg, B., Buetcw, K.H., Schaefer, C.F., Bhat, N.K.,
Altschul, S.F., Zeeberg, B., Buetcw, K.H., Schaefer, C.F., Bat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Mang, J., Haish, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M.M. B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Boastk, S.A., McEwant, F.J.,
Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
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                                                                 Bukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
(Dases 1 to 3707)
Morio, T., Urushihara, H., Saito, T., Ugawa, Y., Mizuno, H., Yoshida, M., Yoshino, R., Mitra, B.N., Pi, M., Sato, T., Takemoto, K., Yasukawa, H., Yoshino, R., Mitra, B.N., Takeuchi, T., Ochiad, H. and Tanaka, Y.
The Dictyostelium developmental cDNA project: generation and analysis of expressed sequence tags from the first-finger stage of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 4097)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="slug"
/clone_lib="Dictyostelium discoideum SS (H.Urushihara)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: hideko@biol.tsukuba.ac.jp
PROJECT = 'Dictyostelium discoideum cDNA project in Japan'
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100.0%; Pred. No. 1.9e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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/organism="Dictyostelium discoideum"

/mol_type="mRNA"

/strain="Ax4"

/db_xref="taxon:44689"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Institute of Biological Sciences
University of Tsukuba
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                                                                                                                                                                                                                                                                                                                                                                      DNA Res. 5 (6), 335-340 (1998)
99156227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Hideko Urushihara
Dictyostelium discoideum
Dictyostelium discoideum
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Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.W., Hong, L., Stapletcn, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Hulyk, S.W., Fahey, J., Helton, E., Ketteman, M., Madan, A., Kodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schwutz, J., Myers, R.M., Butterfield, Y.S., Kzzywinski, M.I., Skalska, U., Smallus, D.E., Schner, J.S., Schein, J.E., Jones, S.J. and Marra, M.A. Genration and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LIML at: http://image.llnl.gov Series: IRAK Plate: 61 Row: b Column: 10 This clone has the following problem: no 5' EST match. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (02-078-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowis, C.R., Sheed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
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4207 bp mRNA linear HTC 19-NC Homo sapiens hypothetical protein LOC90529, mRNA (cDNA clone IMAGE:4827425), containing frame-shift errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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/clone_lib="NCI_CGAP_Mam6"
/lab_host="DH10B"
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100.0%; Pred. No. 1.7e+04;
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/clone="IMAGE:3156629"
/tissue_type="Mammary tumor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Pred. w.
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/organism="Mus musculus"
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/strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center code: BCM-HGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 4168)
Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24; Conservative
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Matches 24; Conserva
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JOURNAL
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BC034315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LINL)
DNA Sequencing by: Baylor College of Medicine Human Genome
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Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 4168)
                                                                                                                                                                                                                                                                                                               Submitted (01-APR-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
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                                                                                                          human and mouse CDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
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100.0%; Pred. No. 1.7e+04;
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Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
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/clone lib="NIH MGC 97"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: amg@bcm.tmc.edu
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                                                                                                                                                                                                                                   (bases 1 to 4097)
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Direct Submission
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BC042403
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HTC 04-MAR-2003

ORGANISM

SOURCE

REFERENCE AUTHORS

ACCESSION

VERSION KEYWORDS

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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: http://image.llnl.gov Series: IRAK Plate: 73 Row: o Column: 3 This clone has the following problem: retained intron. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BC014615 2752 bp mRNA linear HTC 17-DEC-2003
Homo sapiens CDNA clone IMAGE:3532298, containing frame-shift
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tobn Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (31-JU1-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.6%; Score 23; DB 11; Length 2669;
                                                                                                                                                                                                                                      linear
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Best Local Similarity 100.0%; Fred. No. 3.8
                                                                                                                                                                                                                      2669 bp
Homo sapiens, clone IMAGE:5266192,
BC035179
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/clone="IMAGE:5266192"
/tissue_type="Testis"
/clone_lib="NIH_MGC_97"
/lab_host="DH10B"
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                                                                              2376 TGTCAAAAAAAAAAAAAAAAAA 2399
                      3803 TGTCAAAAAAAAAAAAAAAAA 3826
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Klausner, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, R., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Wang, J., Haich, P.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, W.M. B., Bonaldo, M.F., Casarant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Boask, S.A., McEwant, P.J.,
McKernan, K.J., Mallek, J.A., Gunaratne, P.H., Richards, S.W.,
Villalon, D.K., Malk, S.G., Garcia, A.W., Gay, L.J., Hulyk, S.W.,
Fahey, J., Helton, B., Scheim, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J.S., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Generation and initial analysis of more than 15,000 full-length
human and mouse oDNA sequences
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Contact: MGC help desk
Email: ogapbs-rémail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
CDNA Library Arrayed by: The I.M.A.G. E. Consortium (LLNL)
CDNA Library Arrayed by: The I.M.A.G. E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sheed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 4207)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (02-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="DH10B"
/note="Vector: pBluescript"
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/clone lib="NIH MGC 97"
/lab host="DH10B"
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BC034315.1 GI:22832825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 4207)
                                                                                           Homo sapiens (human)
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Best Local Similarity
Matches 24; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2477932
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AUTHORS TITLE JOURNAL

REMARK

COMMENT

MEDLINE PUBMED

JOURNAL

TITLE

REFERENCE

·;

Gaps

·.

source

ORIGIN

FEATURES

(bases 1 to 2752)

REFERENCE

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Mammatais Euchantai Kodentrai Scillogiaciii, muillaas; miniatas Euchantai Kodentrai Scillogia, E. A. Grouse, L. H., Derge, J. G. Klausner, R. L., Collins, F. S., Wagner, L. Shemmen, C. M., Schuler, G. D., Altschul, S. F., Zeeberg, B., Buetow, K. H., Schaefer, C.F., Bhat, N. K., Hopkins, R. F., Jordan, H., Moore, T., Wax, S. I., Wang, J., Haish, F., Diatchenko, L., Marusina, K., Farmer, A. A., Rubin, G. M., Hong, L., Stapleton, M., Soares, M. B., Bonaldo, M. F., Casavant, T. L., Scheetz, T. E., Brownstein, M. J., Usdin, T. B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S. S., Loquellano, N. A., Peters, G. J., Abramson, R. J., Mullahy, S. J., Bosak, S. A., McEward, P. J., McKernan, R. J., Malek, J. A., Garcia, A. M., Gay, L. J., Hulyk, S. W., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Koung, A. C., Shevchenko, Y., Butkesley, R. W., Touchman, J. W., Green, E. D., Dickson, M. C., Rodrigues, M. M., Schein, J. S., Kazywinski, M. I., Skalska, U., Smailus, D. E., Schnerch, A., Schein, J. E., Jones, S. J. and Marra, M. B.
               HTC 19-NOV-2003
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Web site: http://www.nisc.nih.gov/
Contact: nisc_mgcompgri.nih.gov/
Contact: nisc_mgcompgri.nih.gov/
Shkhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Dietrich,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduco,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
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Series: IRAK Plate: 65 Row: i Column: 23
This clone has the following problem: retained intron.
                                                                                                                                                                                                                                                             Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (07-MAY-2002) National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
           linear HTC 15
mRNA (cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue type="Bye, retina, mouse strain C57Bl\6"
/clone_lib="NIH_MGC_94"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
       BC030311
2802 bp mRNA lin
Mus musculus RIKEN cDNA 1200015K23 gene, mRNA
IMAGE:5369232), with apparent retained intron.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human and mouse cDNA sequences
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                                                                                                                                                                                                                               Mus musculus (house mouse)
                                                                                                                                                       BC030311.1 GI:20988454
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           LOCUS
DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
TITLE
JOURNAL
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PUBMED
                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
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                                                                                                                                                       VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
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                                                                                                                                                                                                                                   SOURCE
                                                     Strausberg, L. J. Feingold, E. A., Grouse, L. H., Derge, J. G., Klausberg, R. L., Feingold, E. A., Grouse, L. H., Derge, J. G., Klausner, R. L., Collins, F. S., Wagner, L., Shenmen, C. M., Schuler, G. D., Altschul, S. F., Zeeberg, B., Buetow, K. H., Schaefer, C. F., Bhat, N. K., Hopkins, R. F., Jordan, H., Moore, T. Mara, S. I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K. Parmer, A.A., Rubin, G. M., Hong, L., Stapleton, M., Soares, M. B., Bonaldo, M. F., Casavant, T. I., Scheetz, T. E., Brownstein, M. J., Usdin, F. J. Carninci, P., Prange, C., Raha, S. S., Loquellano, N. A., Peters, G. J., Abramson, R. D., Mullahy, S. J., Bosak, S. A., McEwan, P. J., Mullahy, S. J., Gunaratne, P. H., Richards, S. Worley, K. C., Hale, S., Garcia, A. M., Gay, L. J., Hulyk, S. M. Villalon, D. K., Muzhy, D. M., Sodergren, E. J., Lu, X., Gibbs, R. A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiling, M., Madan, A., Young, A. C., Shevthen, E. Dickson, M. C., Rodriguez, A. C., Grimwood, J., Schmutz, J., Myers, R. M., Generation and initial analysis of more than 15,000 full-length human and mouse cond supplies of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 11 Row: j Column: 11
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 18375616
This clone has the following problem: frame shifted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
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Submitted (24-S2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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On Aug 19, 2003 this sequence version replaced gi:15779097.
Contact: MGC help desk
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Institute for Systems Biology http://www.systemsbiology.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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/tissue type="Muscle, rhabdomyosarcoma"
/tone lib="NIH MGC_17"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
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/db_xref="taxon:9606"
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Tissue Procurement: ATCC
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Matches 23; Conservative

RESULT 15

BC030311

Query Match Best Local Similarity

DRIGIN

source

FEATURES

(bases 1 to 2752)

12477932

JOURNAL REFERENCE

Strausberg, R.

TITLE

AUTHORS

USA

REMARK COMMENT

ORIGIN

/lab\_host="DH10B" /note="Vector: pCMV-SPORT6"

0; Gaps Query Match 0.6%; Score 23; DB 11; Length 2802; Best Local Similarity 100.0%; Pred. No. 3.7e+04; Matches 23; Conservative 0; Mismatches 0; Indels 0;

ga qa

Search completed: September 4, 2004, 13:11:20 Job time : 6098 secs